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GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Tue 28 Jun 105 16:02:25-PST

Solution Parameters:

    Nucleic Alphabet    = Identity
    Output line length  = 80
    Compress            = Off
    Histogram           = Off
    Randomization       = Off

    AMINO-Res-length    = 2
    DELetion-weight     = 5.00
    LEngth-factor       = 0
    Matching-weight     = 1.00
    NUCLBIC-Res-length  = 4
    SPread-factor       = 50

Clustered order of selected sequences:

    6. US-10-788-606-15    (1-532)
    4. US-10-788-606-11    (1-638)
    3. US-10-788-606-9     (1-642)
    5. US-10-788-606-13    (1-674)
    1. US-10-788-606-1     (1-2301)
    2. US-10-788-606-5     (1-2301)

Region Alignment: (listed in Clustered order)
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US-10-788-   1

US-10-788-   1   ATGCAGCcctCACT
US-10-788-   1   ATGCAGCTCccCACT
                                                  |||||||| || ||||
US-10-788-   1   tCTGGCaCCATGCAGCTctCACT
                             |||||||||||||||||||||||||
US-10-788-   1   gagGaccGagtGCccttCCTCCT   AGAGCCGTGTACTGGAAGGTGCGCGTGCCCTCCTTCCTTCTTCTTCTTGGCTGGTACCAGTCCCACT
                    |||||||||||||||||||||||||
US-10-788-   1   AGAGCCCTGTGCTACTGGAAGGTGCGCGTGCCCTCCTTCCTTCTTCTTCTTGGCTGGTACCAGTCCCACT
US-10-788-   1   AGAGCCCTGTGCTACTGGAAGGTGCGCGTGCCCTCCTTCCTTCTTCTTCTTGGCTGGTACCAGTCCCACT
consensus   agagccctgtgctactggaaggtgcgcgtgccctccttccttctggctggtaccagtccccact

US-10-788-   15   aGCCCCcGTGcTTcatCTGCCTacTCTgTtgCACgCtGCCTTCTgtcGTGGCgTGCCGCCCTGCTGCCGTGCtGTGGCGCCC
US-10-788-   15   gGCCCTcGTGtCTTGTCTgGCTGGCTGCCGCAGCGTACCCgGTGGAGGGCCAGGGG
US-10-788-   47   aGCCCCctGcCTTGcCTTGCCTGCTGCTGTACAtgCAgCCTTCgtTgctGTGGAgaGCCAGGGG
US-10-788-   62   GGCCCCTGTGTCGTCTCGTTGCCTGCTGCTGGTACACACAGCCTTCCGTGTAGTGGAGGGCCAGGGG
US-10-788-   62   GGCCCCTGTGTCTCatCTGCCTcatCTGCCTGCTGCTGGTACACACAGCCTTCCGTGTAGTGGAGGGCCAGGGG
consensus   ggccctgtgtcgtctgctcgctggtacacgcagccttccgtgtagtggagggccagggg

US-10-788-   1   aGAATGATGCCACAGAaaTCATCCCcGaGCTgGGCGAGCTgGGCGAGTACCCCGAGC
US-10-788-   76   TGGCAaGCCTTCAgGAATGATGATGCCACAGAggTCATCCCcaGGCTTcgGAGCTCGGCGAGTACCCCCGAGC
US-10-788-   76   TGGCAgGCCTTCAaGAATGATGATGCCACGGAAATCATCCCcGaGCTCGGCGAGTACCCCCGAGC
US-10-788- 108   TGGCAaGCCTTCAaGAATGATGATGCCACaGAAATCATCCCcGgaCTCaGAGTACCCCaGAGC
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US-10-788-  123     TGGCAGGCGGTTCAaGAATGATGATGCCACGCGGAAATCATCCCCGAGAGCTCCGaGAGTAGTACCCCGAGC
                    ||||||||||||||||||||||||||| ||||| ||||||||||| |||  |||||||||||||||||||||
US-10-788-  123     TGGCAGGCGGTTCAaGAATGATGATGCCACGCGGAAATCATCCcgCGAGCTCcgGaGAGTAGTACCCCGAGC
consensus           tggcaggccgttcaagAATGATGATGCCAC-GAaaTCATCCCcGagCTcgGaGAGTAGTACCCCGAGC

US-10-788-   49     CTC       tgccagagctGAACAACaAgACCATGAACCGGCCGGAGAACGGAGGgAGACCTCC
                    |||       |||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  137     CTCC      tCctGAGACAACCAGACCATGAACCGGCCGGAGAATGAGGcAGAGACCTCC
                    ||||      |||| |||||||||||||||||||||||||||||||||||| |||| ||
US-10-788-  137     CTCcaCcGGAgCTgGAGAACAACaGAGACCATGAACCGGCCGGAGAATGGAGGgcGGCaCCTCC
                    ||||      |||| |||||||||||||||||||||||||||||||||||||||||||| |||
US-10-788-  169     CTCCCcCAgGAaCTaGAGACAACCaGACCATGAACCGGCCGGAGAACGGAGGcaGaCCCC
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  184     CTCCACCGGAGCTGGAGAACAACaGACCATGAACCGGCCGGAGAACGGAGGGCGGCCTCC
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
US-10-788-  184     CTCCACCGGAGCTGGAGAACAACaGACCATGAACCGGCCGGAGAACGGAGGGCGGCCTCC
consensus           CTCcaccggagctggaGAACAACaGACCATGAACCGGCCGgAGAACggaGGaGGg-G-CctCC

US-10-788-  107     CCACCACCCTtTGAgaCCAAAGacGccTCCGAGTACAGCTGCCGGGAGCTGCACTtCACC
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  192     CCACCAtCCCTaTACgCCAAAGtGTGTCCCGAGTACAGCTGCCGGaGAGCTGCACTaCACC
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  198     CCACCAcCCCTtTGAgaCCAAAGACGTGTCCCGAGTACAGCTGCCGGaGAGCTGCACTtCACC
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  230     CCACCAtCCCTaTGAtGCcCAAAGACGTGTCCGAGTACAGCTGCCGGaGAGCTGCACTaCACC
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  245     CCACCACCCCTTTGAGACCAAAGACGTGTCCGAGTACAGCTGCCGGaGAGCTGCACTTCACC
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  245     CCACCACCCCTTTGAGACCAAAGACGTGTCCGAGTACAGCTGCCGGaGAGCTGCACTTCACC
consensus           CCACCACcCCTtTGAgaCCAAAGacGtgTCCGAGTACAGCTGCCGGaGAGCTGCACTtcACC

US-10-788-  168     CGCTaCgTGACcGAtGGgCCgGCGCGCCaGTGCCGCAAGGCCAAGCGCGTCACCGAGcTGGTGTGCTCgG
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  253     CGCTtCCTGACaGACGGcGCcCCaTGGCGCCaGTGCCGCAAGGCCAAGCGCGTCACCGAGTTGGTGCTCCG
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  259     CGCTaCgTGACcGAtGGgCCgGCGCaCGcGCGCGGCCGTGCCGCAAGGCCAAGCGCGTCACCGAGTTGGTGTGCTCCG
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  291     CGCTtCgTGACcGAcGGgCCgCGCGCaGcCGCGGCCGTGCCGCAAGGCCAAGCGCGTCACCGAGTTGGTGTGCTCgG
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  306     CGCTaCgTGACcGAtGGgCCgGCGCGCCGCGGCCGTGCCGCAAGGCCAAGCGCGTCACCGAGTTGGTGTGCTCCG
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  306     CGCTaCgTGACcGAtGGgCCgCGCGCCGCGGCCGTGCCGCAAGGCCAAGCGCGTCACCGAGTTGGTGTGCTCCG
consensus           CGCTaCgTGACcGAtGGgCCgGCGCGCCGCGGCCGTGCCGCAAGGCCAAGCGCGTCACCGAG-TGGTGTGCTCcG

US-10-788-  229     GCCAGTGCGGCCCCggCGCgCCTGCTGCCCAACGCCATCGCcGCGTACCGGCAAGGTGGTGGCCCC
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  314     GCCAGTGCGGCCCCggCGCCCGCGGCCTGCTGCCCAACGCCATCGGcGCGTCACCGGGCGCGGCCCC
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  320     GCCAGTGCGGGCCCCgGCaCGcCTGCTGCCCAACGCCATCGGcGCGTACCGGgCAAGGTGGTGGCGCCC
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  352     GCCAGTGCGGCCCCggCTGcTGCTGCCCAACGCCATCGGcGCGTgAAGGTGGTGGCGCGCC
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  367     GCCAGTGCGGCCCCgGCGCgCCTGCTGCCCAACGCCATCGCcGCGTACCGGtGGTGGCGGACC
consensus           GCCAGTGCGGCCCCggCGCgCCTGCTGCCCAACGCCATCGGcGCGTACCGGcaAGGTGGTGGCGccC

US-10-788-  290     aAgCGGgCCcGAcTTCGGCTGcGATCCCcacaccGCTACCCGCGCGAGCGGGTGCAGCTGcTG
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  375     GAaCGGaCCgGAtTTCGGCTGtGAtCCGtcGATcGGcGCTACCCGCGCGAGCTGGGTGCAGCTGCTG
                    ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788-  381     GAgtGGgCCGACTTCCGCGACTTCCCGaccGGCTACCCGaGCTGGGTGCAGCTGCTG
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US-10-788- 413   GAacGGacCCGACTTCCGcTCATCCCgGAtCGcTACCGCGCGGCAGCGgGTGCAGCTGCTG
                 ||   || ||||||||| ||||||||| || || |||||||||||||||| ||||||||||
US-10-788- 428   TAGTGGGCCCcACTTCCGcTCATCCCgGAtCGcTACCGCGCGGCAGCGgGTGCAGCTGCTG
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 428   TAGTGGGCCCcACTTCCGcTCATCCCgGAtCGcTACCGCGCGGCAGCGgGTGCAGCTGCTG
consensus        gAg-GGgCCCgGACTTCCGcTCATCCCgGAccCGcTACCGCGCGGCAGCGgGTGCAGCTGCTG

US-10-788- 351   TGtCCtGGcGGGCGGGGCGCCGCGCGcGCCGCGCtCGCGCAAGGTGCGcCTGTGGCCTCGTGCAAGTGCA
                 ||| || || |||||| ||||||||| || ||| ||||||||||||| |||||||||||||||||||||||
US-10-788- 436   TGcCCCGGgGGGCGGGGCGCCGCGCCGcGCCGCGCtCGCGCAAGGTGCGgCTGTGGCCTCGTGCAAGTGCA
                 ||| ||||| ||||||| || |||||| || ||||||||||||||||| |||||||||||||||||||||||
US-10-788- 442   TGtCCCGGtGtGCGGCGCGCCGCGCGcGCCGCGCtCGCGCAAGGTGCGcCTGTGGCCTCGTGCAAGTGCA
                 ||| |||| | ||||| ||||||||| || ||| ||||||||||||||||||||||||||||||||||||||
US-10-788- 474   TGcCCCGGcGCGGCGGCGCGCCGCGCGcGCCGCGCtCGCGCAAGGTGCGcCTGTGGCCTCGTGCAAGTGCA
                 ||| |||| | ||||| ||||||||| || || ||||||||||||||| |||||||||||||||||||||||
US-10-788- 489   TGTCCCGGTGTGAGGGCGCGGCGCCGCGCGGCGCCGCGCAAGGTGCGcCTGTGGCCTCGTGCAAGTGCA
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 489   TGTCCCGGTGGTGAGGGCGCGGCGCCGCGCGGCGCCGCGCAAGGTGCGcCTGTGGCCTCGTGCAAGTGCA
consensus        TGtCCCgGtGG-GcgGGCGCGGCGCCGCGCGgCGCCGCGCAAGGTGCGcCTGTGGCCTCGTGCGTCAAGTGCA

US-10-788- 412   AGCGCCCTCACTcGCTTCCACAACCAGTCcGAGCTCAAGGACTTCGGGGCCCGCCGGCCGGCGG
                 ||||||||| || |||||||||||||||| |||||||||||||||||||||||||| ||||||||||
US-10-788- 497   AGCGCCCTCACCCGCTTCCACAACCAGTCcGAGCTCAAGGACTTCGGGGCCCGGCCGcGAGaCCGCGCG
                 ||||||||| || |||||||||||||||||||||||||||||||| || ||||| || || || |||||
US-10-788- 503   AGCGCCCTcACCCGCTTCCACAACCAGTCcGAGCTCGAGCTtCGGtCCCGAGGtCCgtCG
                 ||||||| || ||||||||||||||||| ||||||||| ||| || | || ||| || ||
US-10-788- 535   AGCGCCCTcACCCGCTTCCACAACCAGTCcGAGCTCGAGaCCtCGGGACCGGCCGGCGCTCG
                 ||||||| || |||||||||||||||||||||||||| ||| ||| |||| |||||| ||| ||
US-10-788- 550   AGCGCCCTcACCCGCTTCCACAACCAGTCcGAGCTGGAGCTtCGGGACCTCGGGACCGCCGCCGCCCCTCG
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 550   AGCGCGCTCACCCGCTTCCACAACCAGTCcGAGCTGGAGCTtCGGGACTTCGGGGCCCGCCGAGCCGCGC-CG
consensus        AGCGCGCTCACCCGCTTCCACAACCAGTCcGAGCTGGAGCTtCGGGACTTCGGGGCCCGCCGAGCCGCGC-CG

US-10-788- 473   GCCGCCAAACGGGCCGGcGGAGCtCGCGGGCCCCCGGGGCAGCCAAAGCCAgCCGGGCCGA
                 || | ||| ||||| |||| ||| ||| ||| ||||||| |||||||||| ||| || ||||
US-10-788- 558   GCCGCAGAAGGGtCGCAAGCCGGCCCGGGGaGCGCCGGGCCGCCAAAGCCAACCAGGCGGAG
                 ||| ||| || | || |||||| | ||||| || ||||||||||||||| |||| ||||||
US-10-788- 564   GCCGCAGAGAGGGcGGAAGCCGGGCCGGGGGGCGGCGGGCCGCCAAAGCCAAtCAGGCCGAG
                 ||| ||| || | || |||| || |||||| |||| |||||||||||||| || || |||||
US-10-788- 596   GCCGCAGAGGGGtCGCAAGCCGGGCGGGGGGGCGCGGAGCGCCAACCAGGCCGAG
                 || | ||| ||| || |||| ||| ||||| || || ||||||||| || |||||
US-10-788- 611   GCCGCAGAGGGGGCGGAAGCCGGAACGGGCCCCGAGGCGCCAAAGCGCCAACCAGGCCGAG
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 611   GCCGCAgAaGGGCcCGGAAGCCGGcGCGGGCCCGAGGCGcgCCAAAGCCAAcCAgGGCCGAg
consensus        GCCGCAgAaGGGCcCGGAAGCCGGcGCGGGCCCGAGGCGcgCCAAAGCCAAcCAgGGCCGAg

US-10-788- 533
US-10-788- 619   CTGGAGAACGCCTACTAGag
                 ||||||||||||||||||
US-10-788- 625   CTGGAGAACGCCTACTAG
                 ||||||||||||||||||
US-10-788- 657   CTGGAGAACGCCTACTAG
                 ||||||||||||||||||
US-10-788- 672   CTGGAGAACGCCTACTAGAGAGCCCGCCCGCGCCCGCCCTCCCACCGGCGCGCCCGGCCCTG
                 ||||||||||||||||||
US-10-788- 672   CTGGAGAACGCCTACTAGAGAGCCCGCCCGCGCCCGCCCTCCCACCGGCGCGCCCGGCCCTG
consensus        ctggagaacgcctactagagccccgcccgcgcccgcccctcccaccggcgcgcccggccctg

US-10-788- 533
US-10-788- 639
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US-10-788- 643   AACCCGGCGCCCACATTTCTGTCCTCTGCGCGTGGTTTGATTGTTTATATTCATTGTAAA
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 675   AACCCGGCGCCCACATTTCTGTCCTCTGCGCGTGGTTTGATTGTTTATATTCATTGTAAA
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 733   AACCCGGCGCCCACATTTCTGTCCTCTGCGCGTGGTTTGATTGTTTATATTCATTGTAAA
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 733   AACCCGGCGCCCACATTTCTGTCCTCTGCGCGTGGTTTGATTGTTTATATTCATTGTAAA
consensus        aacccggcgcccacatttctgtcctctgcgcgtggtttgattgtttatattcattgtaaa

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 794   TGCCTGCAACCAGGGCAGGGGGCTGAGACCTTCCAGGCCCTGAGGAATCCCGGCGCCGG
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 794   TGCCTGCAACCAGGGCAGGGGGCTGAGACCTTCCAGGCCCTGAGGAATCCCGGCGCCGG
consensus        tgcctgcaaccaggggctgagaccttccaggccctgaggaatcccgaggaatcccgggcgccgg

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 855   CAAGGCCCCCTCAGCTGAGGGTCCACGGGGCAGGGGGCAGGGGGAATTGAGAGT
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 855   CAAGGCCCCCTCAGCTGAGGGTCCACGGGGCAGGGGGCAGGGGGAATTGAGAGT
consensus        caaggcccccctcagccagctgaggggtcccacggggcagggggcagggggaggggaattgagagt

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 916   CACAGACACTGAGCCACGCAGCCCGCCTCTGCGGGCCCGCCTACCTTTGCTGGTTCCCACTTC
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 916   CACAGACACTGAGCCACGCAGCCCGCCTCTGCGGGCCCGCCTACCTTTGCTGGTTCCCACTTC
consensus        cacagacactgagccacgcagcccgcctctgggggccgcctaccttgctggtcccacttc

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 977   AGAGGAGCAGAAATGGAAGCATTTTCACCGCCTGGGTTTTAAGGGAGCGGTGTGGGAG
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 977   AGAGGAGCAGAAATGGAAGCATTTTCACCGCCTGGGTTTTAAGGGAGCGGTGTGGGAG
consensus        agaggaggcagaaatggaagcatttcaccgcctggggtttttaagggagcggtgtgtgggag

US-10-788- 533
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US-10-788-  533
US-10-788-  639
US-10-788-  643
US-10-788-  675
US-10-788- 1343   AAAGAGAGAGAATGAATGCAGTTGCATTGATTGATTCAGTGCCAAGGTCACTTCCAGAATTCAGA
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1343   AAAGAGAGAGAATGAATGCAGTTGCATTGATTGATTCAGTGCCAAGGTCACTTCCAGAATTCAGA
consensus         aaagagagagaatgaatgcagttgcattgattgattcagtgccaaggtcacttccagaattcaga

US-10-788-  533
US-10-788-  639
US-10-788-  643
US-10-788-  675
US-10-788- 1404   GTTGTGATGCTCTTCTGACAGCCAAAGATGAAAAACAAACAGAAAAAAAAAGTAAAGA
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1404   GTTGTGATGCTCTTCTGACAGCCAAAGATGAAAAACAAACAGAAAAAAAAAGTAAAGA
consensus         gttgtgatgctctcttctgacagccaaagatgaaaaacaaacagaaaaaaaaagtaaaga

US-10-788-  533
US-10-788-  639
US-10-788-  643
US-10-788-  675
US-10-788- 1465   GTCTATTTATGGCTGACATATTACGGCTGACAAACTCCTGGAAGAAGCTATGCTGCTTCC
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1465   GTCTATTTATGGCTGACATATTACGGCTGACAAACTCCTGGAAGAAGCTATGCTGCTTCC
consensus         gtctattatggctgacatattacggctgacaaactcctggaagaagctgatgctgcttcc

US-10-788-  533
US-10-788-  639
US-10-788-  643
US-10-788-  675
US-10-788- 1526   CAGCCTGGCTTCCCCGGATGTTTGGCTACCTTCCACCCCTCCATCTCCAAAGAATAACATCA
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1526   CAGCCTGGCTTCCCCGGATGTTTGGCTACCTTCCACCCCTCCATCTCCAAAGAATAACATCA
consensus         cagcctggcttccccggatgtttggctacctccacccctccatctccaaagaataacatca

US-10-788-  533
US-10-788-  639
US-10-788-  643
US-10-788-  675
US-10-788- 1587   TCCATTTGGGGTAGAAAAGGAGAGGGTCCGAGGGTGGTGGGAGGGATAGAAATCACATCCGC
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1587   TCCATTTGGGGTAGAAAAGGAGAGGGTCCGAGGGTGGTGGGAGGGATAGAAATCACATCCGC
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US-10-788-  639
US-10-788-  643
US-10-788-  675
US-10-788- 1038   TGGGAAAGTCCAGGGACTGGTTAAGAAAGTTGGATAAGATTCCCCCTTGCACCTCGCTGCC
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1038   TGGGAAAGTCCAGGGACTGGTTAAGAAAGTTGGATAAGATTCCCCCTTGCACCTCGCTGCC
consensus         tgggaaagtccagggactggttaagaaagttggataagattcccccttgcacctcgctgcc

US-10-788-  533
US-10-788-  639
US-10-788-  643
US-10-788-  675
US-10-788- 1099   CATCAGAAAGCCTGAGGCGTGCCCAGAGCACAAGACTGGGGGCAACTGTAGATGTGGTTTC
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1099   CATCAGAAAGCCTGAGGCGTGCCCAGAGCACAAGACTGGGGGCAACTGTAGATGTGGTTTC
consensus         catcagaaagcctgaggcgtgcccagagcacaagactgggggcaactgtagatgtggtttc

US-10-788-  533
US-10-788-  639
US-10-788-  643
US-10-788-  675
US-10-788- 1160   TAGTCCTGGCTCTGCCACTAACTTGCTGTGTAACCTTGAACTACACAATTCTCCTTCGGGA
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1160   TAGTCCTGGCTCTGCCACTAACTTGCTGTGTAACCTTGAACTACACAATTCTCCTTCGGGA
consensus         tagtcctggctctgccactaacttgctgtgtaaccttgaactacacaattctccttcggga

US-10-788-  533
US-10-788-  639
US-10-788-  643
US-10-788-  675
US-10-788- 1221   CCTCAATTTCCACTTTGTAAAATGAGGGTGGAATAGGATCTCGAGGAGACTATT
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1221   CCTCAATTTCCACTTTGTAAAATGAGGGTGGAATAGGATCTCGAGGAGACTATT
consensus         cctcaatttccactttgtaaaatgagggtggaataggatctcgaggagactatt

US-10-788-  533
US-10-788-  639
US-10-788-  643
US-10-788-  675
US-10-788- 1282   GGCATATGATTCCAAGGACTCCAGGTGCCTTTGAATGGGCAGAGTGAGAGAGAGAG
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1282   GGCATATGATTCCAAGGACTCCAGGTGCCTTTGAATGGGCAGAGTGAGAGAGAGAG
consensus         ggcatatgattccaaggactccaggtgcctttgaatgggcagagtgagagagagagagag
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genalign.rec

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consensus          AGAATATTATTGGGGAAAAACTACAAGTGCTGTGTACATATGCTGAGAAACTGCAGAGCATA
US-10-788- 1892     AGAATATTATTGGGGAAAAACTACAAGTGCTGTGTACATATGCTGAGAAACTGCAGAGCATA
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
consensus          agaatattattggggaaaaactacaagtgctgtacatatgctgagaaactgcagagcata

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675

US-10-788- 1953     ATAGCTGCCACCCAAAATCTTTTTGAAAATCATTTCCAGACAACCTCTTACTTTCTGTGT
US-10-788- 1648     CCCAACTTCCCAAAGAGCAGCATCCCTCCCCGACCCATAGCCATGTTTTAAAGTCACCTT
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 1953     ATAGCTGCCACCCAAAATCTTTTTGAAAATCATTTCCAGACAACCTCTTACTTTCTGTGT
US-10-788- 1648     CCCAACTTCCCAAAGAGCAGCATCCCTCCCCGACCCATAGCCATGTTTTAAAGTCACCTT
consensus          atagctgccacccaaaaatcttttgaaatcatttccagacaacctcttacttctgtgt
consensus          cccaacttcccaaagagcagcagcatccctccccgacccatagcatgtttaaagtcacctt

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675

US-10-788- 2014     AGTTTTTAATTGTTAAAAAAAAAAGTTTTAAACAGAAGCACATGACATGAAAGCCTGC
US-10-788- 1709     CCGAAGAGAAGTGAAAGGTTCAAGGACACTGGCCTTGCAGGCCCGAGGGAGCAGCCATCAC
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 2014     AGTTTTTAATTGTTAAAAAAAAAAGTTTTAAACAGAAGCACATGACATGAAAGCCTGC
US-10-788- 1709     CCGAAGAGAAGTGAAAGGTTCAAGGACACTGGCCTTGCAGGCCCGAGGGAGCAGCCATCAC
consensus          agtttttaattgttaaaaaaaaagtttaaacagaagcacatgacatgaaagcctgc
consensus          ccgaagagaagtgaaaggttcaaggacactggccttgcaggcccgagggagcagccatcac

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675

US-10-788- 2075     AGGACTGGTCGTTTTTTTGGCAATTCTTCCACGTGGACTTGTCCAACAAGAATGAAAGTAG
US-10-788- 1770     AAACTCACAGACCAGCACATCCCTTTGAGACACCGCCTTCTGCCACCACTCACGGACAC
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US-10-788- 2075     AGGACTGGTCGTTTTTTTGGCAATTCTTCCACGTGGACTTGTCCAACAAGAATGAAAGTAG
US-10-788- 1770     AAACTCACAGACCAGCACATCCCTTTGAGACACCGCCTTCTGCCACCACTCACGGACAC
consensus          aggactggtcgttttttgcaattcttccacgtggacttgtccaacaagaatgaaagtag
consensus          aaactcacagaccagcacatccctttgagacaccgccttctgccaccactcacggacac

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675

US-10-788- 2136     TGGTTTTTAAAGAGTAAGTACATATTATTTCTCACTTAAGTTATTTATGCAAAAGTT
US-10-788- 1831     ATTTCTGCCTAGAAAACAGCTTCTTACTGCTCTTACATGTGATGGCATATCTTACACTAAA
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-10-788- 2136     TGGTTTTTAAAGAGTAAGTACATATTATTTCTCACTTAAGTTATTTATGCAAAAGTT
US-10-788- 1831     ATTTCTGCCTAGAAAACAGCTTCTTACTGCTCTTACATGTGATGGCATATCTTACACTAAA
consensus          tggtttttaaagagtaagtacatattattttctcacttaagttattatgcaaaagtt
consensus          atttctgcctagaaaacagcttcttactgctcttacatgtgatggcatatcttacactaaa

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675

US-10-788- 1892     AGAATATTATTGGGGAAAAACTACAAGTGCTGTGTACATATGCTGAGAAACTGCAGAGCATA
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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US-10-788- 2197 TTTCTTGTGTAGAGAATGACAATGTTAATATGCTTTATGAATTAACAGTCTCGTTCTTCCAGA
                ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
US-10-788- 2197 TTTCTTGTGTAGAGAATGACAATGTTAATATTGCTTTATGAATTAACAGTCTCGTTCTTCCAGA

consensus       tttcttgtgtagagaatgacaatgttaatattgctttatgaattaacagtctcgttcttccaga

US-10-788-  533

US-10-788-  639

US-10-788-  643

US-10-788-  675

US-10-788- 2258 GTCCAGAGACATTGTTAATAAAGACAATGAATCATGACCGAAAG
                |||||||||||||||||||||||| |||||||||||||||||||
US-10-788- 2258 GTCCAGAGACATTGTTAATAAAGACAATGAATCATGACCGAAAG

consensus       gtccagagacattgttaataaagacaatgaatcatgaccgaaag
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Alignment score = -28949.00

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3				521	412	-54
4					396	-106
5						-249
6						

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42 ; Search time 10379.5 Seconds
                                      (without alignments)
                                      10741.894 Million cell updates/sec

Title: US-10-788-606-1
Perfect score: 2301
Sequence: 1:agagcctgtgctactggaag.........caatgaatcatgaccgaaag 2301

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422760795 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

Database :   GenEmbl:*
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               2: gb_htg:*
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               8: gb_pl:*
               9: gb_pr:*
              10: gb_ro:*
              11: gb_sts:*
              12: gb_sy:*
              13: gb_un:*
              14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2301	100.0	2301	6	BD251906	Compositi
2	2301	100.0	2301	6	AR258992	Sequence
3	2301	100.0	2301	6	AR267465	Sequence
4	2301	100.0	2301	6	AR371665	Sequence
5	2301	100.0	2323	9	AF326739	Homo sapi
6	2299.4	99.9	2301	6	BD251907	Compositi
7	2299.4	99.9	2301	6	BD251909	Compositi
8	2299.4	99.9	2301	6	AR258993	Sequence
9	2299.4	99.9	2301	6	AR258995	Sequence
10	2299.4	99.9	2301	6	AR267466	Sequence
11	2299.4	99.9	2301	6	AR267468	Sequence
12	2299.4	99.9	2301	6	AR371666	Sequence
13	2299.4	99.9	2301	6	AR371668	Sequence
14	2297.8	99.9	2301	6	BD251908	Compositi
15	2297.8	99.9	2301	6	AR258994	Sequence
16	2297.8	99.9	2301	6	AR267467	Sequence
17	2297.8	99.9	2301	6	AR371667	Sequence
18	2280.6	99.1	2329	6	AX056687	Sequence
19	2280.6	99.1	2329	6	AX574536	Sequence
20	2280.6	99.1	2329	9	AY358627	Homo sapi
21	2273.2	98.8	2296	9	AF331844	Homo sapi
22	2248.2	97.7	2271	6	AX342535	Sequence
23	2047.8	89.0	7099	6	AX342537	Sequence
24	2047.8	89.0	9301	6	BD251915	Compositi
25	2047.8	89.0	9301	6	AR259001	Sequence
26	2047.8	89.0	9301	6	AR267474	Sequence
27	2047.8	89.0	9301	6	AR371674	Sequence
28	2047.8	89.0	21501	9	AR326736	Homo sapi
29	2047.8	89.0	94752	9	AC003098	Homo sapi
30	2035.8	88.5	80117	9	AC055813	Homo sapi
31	1612	70.1	93790	9	AF397423	Homo sapi
32	1066.4	46.3	177744	2	AC073954	Homo sapi
33	839.6	36.5	1154	9	AY358203	Homo sapi
34	759	33.0	759	6	AX323453	Sequence
35	642	27.9	642	6	AR259025	Sequence
36	642	27.9	642	6	AR267498	Sequence
37	642	27.9	642	6	AR371698	Sequence
38	613.2	26.6	642	6	BD251910	Compositi
39	613.2	26.6	642	6	AR258996	Sequence
40	613.2	26.6	642	6	AR267469	Sequence
41	613.2	26.6	642	6	AR371669	Sequence
42	613.2	26.6	642	9	AF326742	Cercopith
43	536.2	23.3	674	6	BD251912	Compositi
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ALIGNMENTS

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LOCUS   BD251906   2301 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION Compositions and methods for increasing bone mineralization.
ACCESSION   BD251906
VERSION   BD251906.1   GI:33061676
KEYWORDS   JP 2002531090-A/1.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2301)
  AUTHORS   Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
            Paeper,B.W., Ness,J.V. and Winkler,D.G.
  TITLE   Compositions and methods for increasing bone mineralization
  JOURNAL   Patent: JP 2002531090-A 1 24-SEP-2002;
            DARWIN DISCOVERY LTD
COMMENT   OS   Homo sapiens (human)
            PN   JP 2002531090-A/1
            PD   24-SEP-2002
            PF   24-NOV-1999 JP 2000585404
            PR   27-NOV-1998 US   60/110283
            PI   MARY E BRUNKOW,DAVID J GALAS,BRIAN KOVACEVICH,JOHN T MULLIGAN,
            PI   BRYAN W PAEPER,JEFFREY VAN NESS,DAVID G WINKLER PC
            PC   C12N15/09,C12N15/09,A01K67/027,A61K31/713,A61K48/00,A61P19/00, PC
            A61P19/02,
            PC   C07K14/47,C07K16/18,C07K19/00,C12N5/10,C12N9/00,C12P21/02, PC
            C12P21/08,
            PC   C12Q1/02,C12Q1/68,G01N33/53,G01N33/53,G01N33/566,C12N15/00, PC
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            PC   C12N5/00
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FEATURES   Location/Qualifiers
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ORIGIN

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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:      June 28, 2005, 15:05:42 ; Search time 8462.86 Seconds
                                        (without alignments)
                                        10349.440 Million cell updates/sec

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Perfect score:  2301
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       34239544 seqs, 1903213470 residues
Total number of hits satisfying chosen parameters:   68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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        7:  gb_est6:*
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        9:  gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
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Result No.		Score	% Query Match	DB	Length	ID	Description
1		1448.2	62.9	3	1475	AF170491	AF170491 Homo sapi
2		1169.6	50.8	1	1177	AF184211	AF184211 Homo sapi
3		668.4	29.0	5	685	BU617598	BU617598 UI-H-DF0-
4		658.2	28.6	5	686	BU621845	BU621845 UI-H-DF0-
5		642	27.9	9	642	AY400962	AY400962 Homo sapi
6		550.4	23.9	9	637	AY400963	AY400963 Pan trogl
7		527.2	22.9	1	1990	AK017295	AK017295 Mus muscu
8		512.4	22.3	6	540	AI768408	AI768408 wh14c03.x
9		506.2	22.0	6	947	BY717106	BY717106 BY717106
10		501.6	21.8	9	636	AY400964	AY400964 Mus muscu
11		494	21.5	2	494	BX282099	BX282099 BX282099
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14		469.4	20.4	2	623	BB637315	BB637315 BB637315
15		457	19.9	2	468	AI498457	AI498457 tm49e03.x
16		452	19.6	1	466	AI383985	AI383985 te35f02.x
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19		419.4	18.2	7	432	CN258789	CN258789 170005325
20		387.4	16.8	1	414	AI498691	AI498691 tm42c02.x
21		375.2	16.3	1	402	AA969408	AA969408 op53b07.s
22		367	15.9	2	511	BB638050	BB638050 BB638050
23		351.8	15.3	2	419	BE101082	BE101082 UI-R-BJ1-
24		341	14.8	1	341	AI580267	AI580267 tm45e09.x
25	c	335	14.6	2	352	BF431247	BF431247 naa42g09.
26	c	321.8	14.0	6	498	CB425970	CB425970 601084 MA
27	c	306.2	13.3	1	360	AI556282	AI556282 UI-R-C2p-
28	c	294	12.8	1	329	AI783624	AI783624 t99d03.x
29	c	278.2	12.1	6	704	CB418651	CB418651 591462 MA
30		264.2	11.5	5	269	CN258788	CN258788 170005328
31	c	260.6	11.3	8	535	AQ171546	AQ171546 HS_3088 B
32	c	256.6	11.2	9	732	CR823295	CR823295 GR0AA53C
33	c	255.8	11.1	1	315	AI113131	AI113131 UI-R-C2p-
34	c	243	10.6	2	291	BE111224	BE111224 UI-R-BJ1-
35	c	233	10.1	7	548	CO620016	CO620016 DG9-202a2
36		229.4	10.0	7	271	D79813	D79813 HUM330C08B
37		219.2	9.5	6	648	CB432800	CB432800 609052 MA
38		190.4	8.3	6	221	CD250782	CD250782 AGENCOURT
39		163.2	7.1	2	532	AL922835	AL922835 AL922835
40		161.2	7.0	1	180	AA393939	AA393939 zv64f09.r
41		158.8	6.9	2	254	BF523030	BF523030 UI-R-C2p-
42		153.8	6.7	2	643	BB221258	BB221258 BB221258
43		153.8	6.7	4	716	BJ712074	BJ712074 BJ712074
44		151.6	6.6	6	423	CB762755	CB762755 AMGNNUC:T
45		150	6.5	2	676	BB212560	BB212560 BB212560

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                            ALIGNMENTS

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LOCUS       AF170491              1475 bp    mRNA    linear   HTC 01-AUG-2003
DEFINITION  Homo sapiens MSTP078 (MST078) mRNA, complete cds.
ACCESSION   AF170491
VERSION     AF170491.1  GI:3337957
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1475)
AUTHORS     Hui,R.T., Qin,B.M., Sheng,H., Liu,Y.Q., Zhao,B., Liu,B., Wang,X.Y.,
            Zhang,Q., Song,L., Gao,Y., Zhang,C.L., Ye,J., Ji,X.J., Liu,B.H.,
            Lu,H., Xu,H.S., Chen,J.Z., Cai,M.Q., Zheng,W.Y., Teng,C.Y., Liu,Q.,
            Yu,L.T., Lin,J., Gong,Q., Zhang,A.M. and Gao,R.L.
TITLE       Homo sapiens normal aorta mRNA MST078
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 1475)
AUTHORS     Hui,R.T., Qin,B.M., Sheng,H., Liu,Y.Q., Zhao,B., Liu,B., Wang,X.Y.,
            Zhang,Q., Song,L., Gao,Y., Zhang,C.L., Ye,J., Ji,X.J., Liu,B.H.,
            Lu,H., Xu,H.S., Chen,J.Z., Cai,M.Q., Zheng,W.Y., Teng,C.Y., Liu,Q.,
            Yu,L.T., Lin,J., Gong,Q., Zhang,A.M. and Gao,R.L.
TITLE       Direct Submission
JOURNAL     Submitted (19-JUL-1999) Molecular Medicine Center for
            Cardiovascular Disease, Cardiovascular Institute, CAMS and PUMC,
            167, Bei Li Shi Lu, Beijing 100037, P.R.China
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ORIGIN

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   June 28, 2005, 14:54:42 ; Search time 1340.09 Seconds
                                     (without alignments)
                          10164.517 Million cell updates/sec

Title:          US-10-788-606-1
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                Gapop 10.0 , Gapext 1.0

Searched:       439206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:        8780412

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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4	2299.4	99.9	2301	3	AAA29061	Aaa29061 Mutant hu
5	2299.4	99.9	2301	3	AAA29062	Aaa29062 Human TGF
6	2299.4	99.9	2301	13	ADS12964	Ads12964 TGF-beta
7	2299.4	99.9	2301	13	ADS12960	Ads12960 TGF-beta
8	2297.8	99.9	2301	3	AAA29056	Aaa29056 Human TGF
9	2297.8	99.9	2301	13	ADS12962	Ads12962 TGF-beta
10	2280.6	99.1	2301	4	AAA91023	Aaa91023 Human sec
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12	2280.6	99.1	2329	9	ADA01331	Ada01331 Human PRO
13	2280.6	99.1	2329	9	ADA43760	Ada43760 Human CDN
14	2280.6	99.1	2329	9	ADA43528	Ada43528 Human CDN
15	2280.6	99.1	2329	9	ADA01203	Ada01203 Human PRO
16	2280.6	99.1	2329	9	ADA01087	Ada01087 Human CDN
17	2280.6	99.1	2329	9	ADA43644	Ada43644 Human CDN
18	2280.6	99.1	2329	9	ADA06906	Ada06906 Human PRO
19	2280.6	99.1	2329	9	ADA08394	Ada08394 Novel hum
20	2280.6	99.1	2329	9	ADB99687	Adb99687 Human PRO
21	2280.6	99.1	2329	9	ADB86970	Adb86970 Human PRO
22	2280.6	99.1	2329	9	ADB66125	Adb66125 Human CDN
23	2280.6	99.1	2329	10	ADB99803	Adb99803 Human PRO
24	2280.6	99.1	2329	10	ADB99458	Adb99458 Novel hum
25	2280.6	99.1	2329	10	ADB66009	Adb66009 Human CDN
26	2280.6	99.1	2329	10	ADC23407	Adc23407 Human CDN
27	2280.6	99.1	2329	10	ADC26100	Adc26100 Human PRO
28	2280.6	99.1	2329	10	ADE04927	Ade04927 Human PRO
29	2280.6	99.1	2329	10	ADE11233	Ade11233 Human PRO
30	2280.6	99.1	2329	10	ADD88164	Add88164 Human PRO
31	2280.6	99.1	2329	10	ADD95459	Add95459 Human CDN
32	2280.6	99.1	2329	10	ADE06389	Ade06389 Human PRO
33	2280.6	99.1	2329	10	ADE38164	Ade38164 Human PRO
34	2280.6	99.1	2329	10	ADD88280	Add88280 Human PRO
35	2280.6	99.1	2329	10	ADD90861	Add90861 Human CDN
36	2280.6	99.1	2329	10	ADF99416	Adf99416 Human CDN
37	2280.6	99.1	2329	10	ADG06509	Adg06509 Human PRO
38	2280.6	99.1	2329	10	ADG05460	Adg05460 Human PRO
39	2280.6	99.1	2329	10	ADG82461	Adg82461 Human PRO
40	2280.6	99.1	2329	12	ADE51714	Ade51714 Human CDN
41	2280.6	99.1	2329	12	ADE51830	Ade51830 Human CDN
42	2280.6	99.1	2329	12	ADE37688	Ade37688 Human CDN
43	2280.6	99.1	2329	12	ADE37572	Ade37572 Human CDN
44	2280.6	99.1	2329	12	ADD95343	Add95343 Human CDN
45	2280.6	99.1	2329	12	ADE38043	Ade38043 Human PRO

ALIGNMENTS

```
RESULT 1
AAA29055
ID   AAA29055 standard; cDNA; 2301 BP.
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AC   AAA29055;
XX
DT   12-SEP-2000  (first entry)
XX
DE   Human TGF-beta binding protein (BBER) cDNA.
XX
KW   osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
KW   BBER; chromosome 17q12-21; gene therapy; antisense therapy; fracture;
KW   bone mineralization; BB.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             48..689
FT                   /tag= a
FT                   /product= "TGF-beta_binding_protein"
XX
PN   WO200032773-A1.
XX
PD   08-JUN-2000.
XX
PF   24-NOV-1999;  99WO-US027990.
XX
PR   27-NOV-1998;  98US-0110283P.
XX
PA   (DARW-) DARWIN DISCOVERY LTD.
XX
PI   Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW;
PI   Van Ness J, Winkler DG;
XX
DR   WPI; 2000-412321/35.
DR   P-PSDB; AAY96429.
XX
PT   Nucleic acids (I) encoding a transforming growth factor beta binding
PT   protein, useful for identifying agents for treating osteopenia,
PT   osteoporosis and fractures.
XX
PS   Claim 1; Page 114-115; 162pp; English.
XX
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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    June 28, 2005, 15:15:06 ; Search time 1539.09 Seconds
                              (without alignments)
                              9344.794 Million cell updates/sec

Title:         US-10-788-606-1
Perfect score: 2301
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Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters:    12134778

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                    Published Applications NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.   Score  Match  Length DB ID                       Description
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 2    2301   100.0  2301   17  US-10-463-190-1           Sequence 1, Appli
 3    2301   100.0  2301   18  US-10-095-248A-1          Sequence 1, Appli
 4    2301   100.0  2301   19  US-10-788-606-1           Sequence 1, Appli
 5    2301   100.0  2301   21  US-10-799-162-1           Sequence 1, Appli
 6    2301   100.0  2301   21  US-10-868-497-57          Sequence 57, Appl
 7    2301   100.0  2323   17  US-10-377-315-2           Sequence 2, Appli
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 12  2299.4  99.9  2301  18  US-10-095-248A-3    Sequence 3, Appli
 13  2299.4  99.9  2301  18  US-10-095-248A-7    Sequence 7, Appli
 14  2299.4  99.9  2301  19  US-10-788-606-3     Sequence 3, Appli
 15  2299.4  99.9  2301  19  US-10-788-606-7     Sequence 7, Appli
 16  2299.4  99.9  2301  21  US-10-799-162-3     Sequence 3, Appli
 17  2299.4  99.9  2301  21  US-10-799-162-7     Sequence 7, Appli
 18  2299.4  99.9  2301  21  US-10-868-497-61    Sequence 61, Appl
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 25  2280.6  99.1  2329  14  US-10-245-859-63    Sequence 63, Appl
 26  2280.6  99.1  2329  17  US-10-245-752-63    Sequence 63, Appl
 27  2280.6  99.1  2329  14  US-10-245-103-63    Sequence 63, Appl
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 29  2280.6  99.1  2329  14  US-10-245-143-63    Sequence 63, Appl
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 37  2280.6  99.1  2329  14  US-10-245-055-63    Sequence 63, Appl
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ALIGNMENTS

RESULT 1
US-10-384-893-1
; Sequence 1, Application US/10384893
; Publication No. US20030166247A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
; TITLE OF INVENTION: BONE MINERALIZATION
; FILE REFERENCE: 240083.508D5
; CURRENT APPLICATION NUMBER: US/10/384,893
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-384-893-1

  Query Match   100.0%; Score 2301; DB 16; Length 2301;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 2301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 AGAGCCTGTGCTACTGAAGGTGGCGTGCCCTCCTCTGGCTGGTACCATGCAGCTCCCAC 60

OM nucleic - nucleic search, using sw model

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Run on: June 28, 2005, 14:55:24 ; Search time 9974.03 Seconds
                               (without alignments)
                               9417.841 Million cell updates/sec

Title: US-10-788-606-1
Perfect score: 2301
Sequence: 1 agagcctgtgctactggaag........caatgaatcatgaccgaaag 2301

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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              GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          June 28, 2005, 14:55:24 ; Search time 1618.95 Seconds
                                            (without alignments)
                                 6348.430 Million cell updates/sec

Title:           US-10-788-606-1
Perfect score:   2301
Sequence:        1 agagcctgctactggaag........caatgaatcatgaccgaaag 2301

Scoring table:   IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        13027057 seqs, 223325459 residues

Total number of hits satisfying chosen parameters:    26054114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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3		570	24.8	570	15	US-60-677-583-99	Sequence 99, Appl
4		73.6	3.2	1089	15	US-60-680-544-23752	Sequence 23752, A
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6		69.6	3.0	2337	1	PCT-US05-13260-1	Sequence 1, Appli
7	c	60.6	2.6	39723	11	US-10-990-328A-96899	Sequence 96899, A
8		55.8	2.4	1216	15	US-60-669-241-24312	Sequence 24312, A
9		53.2	2.3	604	9	US-10-703-032-100242	Sequence 100242,
10		53	2.3	1149	7	US-10-990-000-13	Sequence 13, Appl
11	c	52.4	2.3	1917	9	US-10-703-032-28735	Sequence 28735, A
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14		52.2	2.3	3204	8	US-10-450-763-15861	Sequence 15861, A
15		52.2	2.3	5114	8	US-10-450-763-25123	Sequence 25123, A
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18	c	51.4	2.2	4830849	2	PCT-IB03-06509-1355	Sequence 1355, Ap
19		51	2.2	152132	11	US-10-940-774A-13845	Sequence 13845, A
20		51	2.2	152145	11	US-10-940-774A-12371	Sequence 12371, A
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27	c	50	2.2	1103	15	US-60-669-175-7216	Sequence 7216, Ap
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; Sequence 44583, Application US/6680544
; GENERAL INFORMATION:
;   APPLICANT: Cooper, Matthew
;   APPLICANT: Kinch, Deborah
;   APPLICANT: Rosenberg, Michael
;   APPLICANT: Subramaniam, S. Sai
;   APPLICANT: Szak, Suzanne
;   APPLICANT: Li, Huo
;   APPLICANT: Bandaru, Raj
;   APPLICANT: Derbel, Maher
;   TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
;   TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
;   FILE REFERENCE: 21590290000
;   CURRENT APPLICATION NUMBER: US/60/680,544
;   CURRENT FILING DATE: 2005-05-13
;   NUMBER OF SEQ ID NOS: 48714
;   SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 44583
;   LENGTH: 2302
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-60-680-544-44583

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            Copyright (c) 1993 - 2005  Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a
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31	536.2	23.3	674	4	US-09-668-021-13	Sequence 13, Appl
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33	502	21.8	638	4	US-09-668-529A-11	Sequence 11, Appl
34	502	21.8	638	4	US-09-668-037A-11	Sequence 11, Appl
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                        ALIGNMENTS

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; Patent No. 6395511
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR INCREASING
; TITLE OF INVENTION:  BONE MINERALIZATION
; FILE REFERENCE: 240083.508
; CURRENT APPLICATION NUMBER: US/09/449,218D
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 45
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         Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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8	2299.4	99.9	2301	6	AR371668	AR371668 Sequence
9	2299.4	99.9	2301	6	BD251906	BD251906 Compositi
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32 c	1066.4	46.3	177744	2	AC073954	AC073954 Homo sapi
33	836.4	36.3	1154	6	AY358203	AY358203 Homo sapi
34	755.8	32.8	759	6	AX323453	AX323453 Sequence
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VERSION     BD251908.1  GI:33061678
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2301)
AUTHORS     Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
            Paeper,B.W., Ness,J.V. and Winkler,D.G.
TITLE       Compositions and methods for increasing bone mineralization
JOURNAL     Patent: JP 2002531090-A 3 24-SEP-2002;
            DARWIN DISCOVERY LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002531090-A/3
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            PR   27-NOV-1998 US   60/110283
            PI   MARY E BRUNKOW,DAVID J GALAS,BRIAN KOVACEVICH,JOHN T MULLIGAN,
            PI   BRYAN W PAEPER,JEFFREY VAN NESS,DAVID G WINKLER PC
            C12N15/09,C12N15/09,A01K67/027,A61K31/713,A61K48/00,A61P19/00, PC
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          9:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Match	Query Match	Length	DB	ID	Description
	1	1448.2	62.9		1475	3	AF170491	AF170491 Homo sapi
	2	1169.6	50.8		1177	3	AF184211	AF184211 Homo sapi
c	3	668.4	29.0		685	5	BU617598	BU617598 UI-H-DF0-
c	4	658.2	28.6		686	5	BU621845	BU621845 UI-H-DF0-
	5	638.8	27.8		642	9	AY400962	AY400962 Homo sapi
	6	547.2	23.8		637	9	AY400963	AY400963 Pan trogl
	7	527.2	22.9		1990	3	AK017295	AK017295 Mus muscu
c	8	512.4	22.3		540	1	AI768408	AI768408 wh14c03.x
c	9	506.2	22.0		947	6	BY717106	BY717106 BY717106
	10	501.6	21.8		636	9	AY400964	AY400964 Mus muscu
	11	491.2	21.3		667	2	BB636457	BB636457 BB636457
c	12	491	21.3	491		2	BX282099	BX282099 BX282099
	13	490.8	21.3		494	5	BB637315	BB637315 BB637315
	14	469.4	20.4		623	2	AI498457	AI498457 tm49e03.x
c	15	457	19.9		468	1	AI383985	AI383985 te35f02.x
	16	452	19.6		466	1	AI493134	AI493134 qz50b02.x
c	17	439.8	19.1		466	1	AA393768	AA393768 zv64f08.8
c	18	428.4	18.6		452	1	CN258789	CN258789 170005325
	19	419.4	18.2		432	7	AI498691	AI498691 tm42c02.x
c	20	387.4	16.8		414	1	AA969408	AA969408 op53b07.8
c	21	375.2	16.3		402	1	BB638050	BB638050 BB638050
	22	367	15.9		511	2	BE101082	BE101082 UI-R-BJ1-
c	23	351.8	15.3		419	2	AI580267	AI580267 tm45e09.x
c	24	341	14.8	341		1		
c	25	335	14.6	25	352	2	BF431247	BF431247 naa42g09.
c	26	321.8	14.0	25	498	6	CB425970	CB425970 601084 MA
c	27	306.2	13.3	25	360	1	AI556282	AI556282 UI-R-C2p-
c	28	294	12.8	25	329	1	AI783624	AI783624 t99d03.x
	29	278.2	12.1	25	704	6	CB418651	CB418651 591462 MA
	30	264.2	11.5	25	269	7	CN258788	CN258788 170005328
c	31	257.4	11.2	25	535	8	AQ171546	AQ171546 HS_3088_B
c	32	256.6	11.2	25	732	9	CR823295	CR823295 GROAAA53C
c	33	255.8	11.1	25	315	1	AI113131	AI113131 UI-R-C2p-
c	34	243	10.6	25	291	2	BE111224	BE111224 UI-R-BJ1-
c	35	233	10.1	25	548	7	CO620016	CO620016 DG9-202a2
	36	229.4	10.0	25	271	7	D79813	D79813 HUM330C08B
	37	219.2	9.5	25	648	6	CB432800	CB432800 609052 MA
	38	190.4	8.3	25	221	6	CD250782	CD250782 AGENCOURT
	39	161.6	7.0	25	532	1	AL922835	AL922835 AL922835
	40	161.2	7.0	25	180	1	AA393999	AA393999 zv64f09.r
	41	155.6	6.8	25	254	2	BF523030	BF523030 UI-R-C2p-
	42	153.8	6.7	25	643	2	BB221258	BB221258 BB221258
	43	153.8	6.7	25	716	4	BJ712074	BJ712074 BJ712074
	44	150	6.5	25	676	2	BB212560	BB212560 BB212560
	45	148.4	6.4	25	423	6	CB762755	CB762755 AMGNNUC:T

ALIGNMENTS

```
RESULT 1
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LOCUS       AF170491               1475 bp    mRNA    linear   HTC 01-AUG-2003
DEFINITION  Homo sapiens MST078 (MST078) mRNA, complete cds.
ACCESSION   AF170491
VERSION     AF170491.1  GI:3337957
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1475)
AUTHORS     Hui,R.T., Qin,B.M., Sheng,H., Liu,Y.Q., Zhao,B., Liu,B., Wang,X.Y.,
            Zhang,Q., Song,L., Gao,Y., Zhang,C.L., Ye,J., Ji,X.J., Liu,B.H.,
            Lu,H., Xu,H.S., Chen,J.Z., Cai,M.Q., Zhang,W.Y., Teng,C.Y., Liu,Q.,
            Yu,L.T., Lin,J., Gong,Q., Zhang,A.M. and Gao,R.L.
TITLE       Homo sapiens normal aorta mRNA MST078
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 1475)
AUTHORS     Hui,R.T., Qin,B.M., Sheng,H., Liu,Y.Q., Zhao,B., Liu,B., Wang,X.Y.,
            Zhang,Q., Song,L., Gao,Y., Zhang,C.L., Ye,J., Ji,X.J., Liu,B.H.,
            Lu,H., Xu,H.S., Chen,J.Z., Cai,M.Q., Zhang,W.Y., Teng,C.Y., Liu,Q.,
            Yu.L.T., Lin,J., Gong,Q., Zhang,A.M. and Gao,R.L.
TITLE       Direct Submission
JOURNAL     Submitted (19-JUL-1999) Molecular Medicine Center for
            Cardiovascular Disease, Cardiovascular Institute, CAMS and PUMC,
            167, Bei Li Shi Lu, Beijing 100037, P.R.China
FEATURES             Location/Qualifiers
     source          1..1475
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="aorta"
     gene            1..1475
                     /gene="MST078"
     CDS             275..601
                     /gene="MST078"
                     /codon_start=1
                     /product="MST078"
                     /protein_id="AAQ13601.1"
                     /db_xref="GI:3333795B"
                     /translation="MRRAQSTRLGATVDVVSSPGSATNLLCNLELHNSPSGPQFPLCK
                     MRVEVGIGSRGDYWHMIPRTPVPFEWAEVRERERKRENECSCIDSVPRSLPEFRVML
                     SSDSQR"
ORIGIN

Query Match            62.9%;    Score 1448.2;    DB 3;    Length 1475;
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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:        June 28, 2005, 14:54:42 ; Search time 1340.09 Seconds
                                         (without alignments)
                              10164.517 Million cell updates/sec

Title:         US-10-788-606-5
Perfect score: 2301
Sequence:      1 agagccctgctgctactggaag........caatgaatcatgaccgaaag 2301

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:      8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    N_Geneseq_16Dec04:*
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           2: geneseqm1990s:*
           3: geneseqm2000s:*
           4: geneseqm2001as:*
           5: geneseqm2001bs:*
           6: geneseqm2002as:*
           7: geneseqm2002bs:*
           8: geneseqm2003as:*
           9: geneseqm2003bs:*
          10: geneseqm2003cs:*
          11: geneseqm2003ds:*
          12: geneseqm2004as:*
          13: geneseqm2004bs:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2301	100.0	2301	3	AAA29056	Aaa29056 Human TGF
2	2301	100.0	2301	13	ADS12962	Ads12962 TGF-beta
3	2299.4	99.9	2301	3	AAA29062	Aaa29062 Human TGF
4	2299.4	99.9	2301	13	ADS12964	Ads12964 TGF-beta
5	2297.8	99.9	2301	3	AAA29055	Aaa29055 Human TGF
6	2297.8	99.9	2301	13	ADS12958	Ads12958 TGF-beta
7	2297.8	99.9	2323	10	ACF79824	Acf79824 Human SOS
8	2296.2	99.8	2301	3	AAA29061	Aaa29061 Mutant hu
9	2296.2	99.8	2301	13	ADS12960	Ads12960 TGF-beta
10	2277.4	99.0	2329	4	AAA91023	Aaa91023 Human sec
11	2277.4	99.0	2329	6	ABK69992	Abk69992 cDNA enco
12	2277.4	99.0	2329	9	ADA01331	Ada01331 Human PRO
13	2277.4	99.0	2329	9	ADA43760	Ada43760 Human CDN
14	2277.4	99.0	2329	9	ADA43528	Ada43528 Human CDN
15	2277.4	99.0	2329	9	ADA01203	Ada01203 Human PRO
16	2277.4	99.0	2329	9	ADA01087	Ada01087 Human CDN
17	2277.4	99.0	2329	9	ADA43644	Ada43644 Human CDN
18	2277.4	99.0	2329	9	ADA06906	Ada06906 Human PRO
19	2277.4	99.0	2329	9	ADA08394	Ada08394 Novel hum
20	2277.4	99.0	2329	9	ADB99687	Adb99687 Human PRO

21	2277.4	99.0	2329	9	ADB86970	Adb86970 Human PRO
22	2277.4	99.0	2329	9	ADB66125	Adb66125 Human CDN
23	2277.4	99.0	2329	10	ADB99803	Adb99803 Human PRO
24	2277.4	99.0	2329	10	ADB99458	Adb99458 Novel hum
25	2277.4	99.0	2329	10	ADB66009	Adb66009 Human CDN
26	2277.4	99.0	2329	10	ADC23407	Adc23407 Human CDN
27	2277.4	99.0	2329	10	ADC26100	Adc26100 Human PRO
28	2277.4	99.0	2329	10	ADE04927	Ade04927 Human PRO
29	2277.4	99.0	2329	10	ADE11233	Ade11233 Human PRO
30	2277.4	99.0	2329	10	ADD88164	Add88164 Human PRO
31	2277.4	99.0	2329	10	ADD95459	Add95459 Human CDN
32	2277.4	99.0	2329	10	ADE06389	Ade06389 Human PRO
33	2277.4	99.0	2329	10	ADE38164	Ade38164 Human PRO
34	2277.4	99.0	2329	10	ADD88280	Add88280 Human PRO
35	2277.4	99.0	2329	10	ADD90861	Add90861 Human CDN
36	2277.4	99.0	2329	10	ADF99416	Adf99416 Human CDN
37	2277.4	99.0	2329	10	ADG06509	Adg06509 Human PRO
38	2277.4	99.0	2329	10	ADG05460	Adg05460 Human PRO
39	2277.4	99.0	2329	10	ADG82461	Adg82461 Human PRO
40	2277.4	99.0	2329	12	ADE51714	Ade51714 Human CDN
41	2277.4	99.0	2329	12	ADE51830	Ade51830 Human CDN
42	2277.4	99.0	2329	12	ADE37688	Ade37688 Human CDN
43	2277.4	99.0	2329	12	ADE37572	Ade37572 Human CDN
44	2277.4	99.0	2329	12	ADD95343	Add95343 Human CDN
45	2277.4	99.0	2329	12	ADE38043	Ade38043 Human PRO

ALIGNMENTS

```
RESULT 1
AAA29056
ID   AAA29056 standard; cDNA; 2301 BP.
XX
AC   AAA29056;
XX
DT   12-SEP-2000  (first entry)
XX
DE   Human TGF-beta binding protein (BEBR) variant V10I cDNA.
XX
KW   osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
KW   BEBR; variant; V10I; gene therapy; antisense therapy; fracture;
KW   chromosome 17q12-21; bone mineralization; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             48..689
FT                   /*tag= a
FT                   /label= BEBR variant V10I
FT                   /product= "TGF-beta_binding_protein"
XX
PN   WO200032773-A1.
XX
PD   08-JUN-2000.
XX
PF   24-NOV-1999;  99WO-US027990.
XX
PR   27-NOV-1998;  98US-0110283P.
XX
PA   (DARW-) DARWIN DISCOVERY LTD.
XX
PI   Brunkow ME,  Galas DJ,  Kovacevich B,  Mulligan JT,  Paeper BW;
PI   Van Ness J,  Winkler DG;
XX
DR   WPI; 2000-412321/35.
DR   P-PSDB; AAY96430.
XX
PT   Nucleic acids (I) encoding a transforming growth factor beta binding
PT   protein, useful for identifying agents for treating osteopenia,
PT   osteoporosis and fractures.
XX
PS   Claim 1; Page 118-119; 162pp; English.
```

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              GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:   June 28, 2005, 15:15:06 ; Search time 1539.09 Seconds
                                    (without alignments)
                         9344.794 Million cell updates/sec

Title:          US-10-788-606-5
Perfect score:  2301
Sequence:       1 agagcctgtgctactggaag........caatgaatcatgaccgaaag 2301

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters:      12134778

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications NA:*
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     2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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     6:  /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
     7:  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
     8:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
     9:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
    10:  /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
    11:  /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
    12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
    13:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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    16:  /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	2301	100.0	2301	17	US-10-463-190-5	Sequence 5, Appli
3	2301	100.0	2301	18	US-10-095-248A-5	Sequence 5, Appli
4	2301	100.0	2301	19	US-10-788-606-5	Sequence 5, Appli
5	2301	100.0	2301	21	US-10-799-162-5	Sequence 5, Appli
6	2301	100.0	2301	21	US-10-868-497-59	Sequence 59, Appli
7	2299.4	99.9	2301	16	US-10-384-893-7	Sequence 7, Appli
8	2299.4	99.9	2301	17	US-10-463-190-7	Sequence 7, Appli
9	2299.4	99.9	2301	18	US-10-095-248A-7	Sequence 7, Appli
10	2299.4	99.9	2301	21	US-10-788-606-7	Sequence 7, Appli
11	2299.4	99.9	2301	21	US-10-799-162-7	Sequence 7, Appli
12	2299.4	99.9	2301	21	US-10-868-497-61	Sequence 61, Appli
13	2297.8	99.9	2301	16	US-10-384-893-1	Sequence 1, Appli
14	2297.8	99.9	2301	17	US-10-463-190-1	Sequence 1, Appli
15	2297.8	99.9	2301	19	US-10-095-248A-1	Sequence 1, Appli
16	2297.8	99.9	2301	19	US-10-788-606-1	Sequence 1, Appli
17	2297.8	99.9	2301	21	US-10-799-162-1	Sequence 1, Appli
18	2297.8	99.9	2301	21	US-10-868-497-57	Sequence 57, Appli
19	2297.8	99.9	2323	17	US-10-377-315-2	Sequence 2, Appli
20	2296.2	99.8	2301	16	US-10-384-893-3	Sequence 3, Appli
21	2296.2	99.8	2301	17	US-10-463-190-3	Sequence 3, Appli
22	2296.2	99.8	2301	18	US-10-095-248A-3	Sequence 3, Appli
23	2296.2	99.8	2301	19	US-10-788-606-3	Sequence 3, Appli
24	2296.2	99.8	2301	21	US-10-799-162-3	Sequence 3, Appli
25	2277.4	99.0	2329	14	US-10-245-752-63	Sequence 63, Appli
26	2277.4	99.0	2329	14	US-10-245-859-63	Sequence 63, Appli
27	2277.4	99.0	2329	14	US-10-245-103-63	Sequence 63, Appli
28	2277.4	99.0	2329	14	US-10-245-107-63	Sequence 63, Appli
29	2277.4	99.0	2329	14	US-10-245-143-63	Sequence 63, Appli
30	2277.4	99.0	2329	14	US-10-245-771-63	Sequence 63, Appli
31	2277.4	99.0	2329	14	US-10-245-851-63	Sequence 63, Appli
32	2277.4	99.0	2329	14	US-10-245-883-63	Sequence 63, Appli
33	2277.4	99.0	2329	14	US-10-237-535-63	Sequence 63, Appli
34	2277.4	99.0	2329	14	US-10-238-183-63	Sequence 63, Appli
35	2277.4	99.0	2329	14	US-10-238-283-63	Sequence 63, Appli
36	2277.4	99.0	2329	14	US-10-238-370-63	Sequence 63, Appli
37	2277.4	99.0	2329	14	US-10-245-055-63	Sequence 63, Appli
38	2277.4	99.0	2329	14	US-10-245-147-63	Sequence 63, Appli
39	2277.4	99.0	2329	14	US-10-245-730-63	Sequence 63, Appli
40	2277.4	99.0	2329	14	US-10-245-739-63	Sequence 63, Appli
41	2277.4	99.0	2329	14	US-10-246-210-63	Sequence 63, Appli
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43	2277.4	99.0	2329	14	US-10-243-024-63	Sequence 63, Appli
44	2277.4	99.0	2329	14	US-10-243-409-63	Sequence 63, Appli
45	2277.4	99.0	2329	14	US-10-245-621-63	Sequence 63, Appli

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

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RESULT 1
US-10-384-893-5
; Sequence 5, Application US/10384893
; Publication No. US2003016247A1
; GENERAL INFORMATION:
;  APPLICANT: Brunkow, Mary E.
;  APPLICANT: Galas, David J.
;  APPLICANT: Kovacevich, Brian
;  APPLICANT: Mulligan, John T.
;  APPLICANT: Paeper, Bryan W.
;  APPLICANT: Van Ness, Jeffrey
;  APPLICANT: Winkler, David G.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
;  TITLE OF INVENTION: BONE MINERALIZATION
;  FILE REFERENCE: 240083.508D5
;  CURRENT APPLICATION NUMBER: US/10/384,893
;  CURRENT FILING DATE: 2003-03-06
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;  LENGTH: 2301
;  TYPE: DNA
;  ORGANISM: Homo sapien
US-10-384-893-5

Query Match             100.0%;  Score 2301;  DB 16;  Length 2301;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2301; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy          1 AGAGCCTGTGCTACTGGAAGGTGGCGTGCCCTCCTCTCGGCTGGTACCATGCAGCTCCCAC 60
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:55:24 ; Search time 9974.03 Seconds
                                         (without alignments)
                                         9417.841 Million cell updates/sec

Title: US-10-788-606-5
Perfect score: 2301
Sequence: 1 agagcctgtgctactggaag.........caatgaatcatgaccgaaag 2301

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 2041152I753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Pending_Patents_NA_Main:*
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    3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
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OM nucleic - nucleic search, using sw model

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8		55.8	2.4	1216	15	US-60-669-241-24312	Sequence 24312, A
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; APPLICANT: Cooper, Matthew
; APPLICANT: Kinch, Deborah
; APPLICANT: Rosenberg, Michael
; APPLICANT: Subramaniam, S. Sai
; APPLICANT: Szak, Suzanne
; APPLICANT: Li, Huo
; APPLICANT: Bandaru, Raj
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
; TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
; FILE REFERENCE: 21590290000
; CURRENT APPLICATION NUMBER: US/60/680,544
; CURRENT FILING DATE: 2005-05-13
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; SOFTWARE: Patent Sequence Analysis Tool Version 1.0
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; LENGTH: 2302
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-60-680-544-44583

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        Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

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42	372.2	16.2		4	US-09-668-037A-17	Sequence 17, Appl
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44	190.2	8.3		4	US-09-513-999C-9816	Sequence 9816, Ap
45	82.6	3.6		3	US-09-188-930-40	Sequence 40, Appl

ALIGNMENTS

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RESULT 1
US-09-449-218D-5
; Sequence 5, Application US/09449218D
; Patent No. 6395511
; GENERAL INFORMATION:
;  APPLICANT: Brunkow, Mary E.
;  APPLICANT: Galas, David J.
;  APPLICANT: Kovacevich, Brian
;  APPLICANT: Mulligan, John T.
;  APPLICANT: Paeper, Bryan W.
;  APPLICANT: Van Ness, Jeffrey
;  APPLICANT: Winkler, David G.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
;  TITLE OF INVENTION: BONE MINERALIZATION
;  FILE REFERENCE: 240083.508
;  CURRENT APPLICATION NUMBER: US/09/449,218D
;  CURRENT FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;  LENGTH: 2301
;  TYPE: DNA
;  ORGANISM: Homo sapien
US-09-449-218D-5

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  Matches 2301;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 TGGCCCTGTGTCTCATCTGCCTGCTGGTACACACGGAAATCATCCGCGAGCTCGGAGTACCAGG 120
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Qy        181 AGCCTCCACCGGAGCTGGAGAACAACAAGACCATGAACCGGCGGAGAACCGGAGGGGCGGC 240
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                GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    June 28, 2005, 14:54:42 ; Search time 2895.97 Seconds
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Title:      US-10-788-606-9
Perfect score: 642
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:   4708233 seqs, 2422760795 residues

Total number of hits satisfying chosen parameters:   9416466

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Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	642	100.0	642	6	BD251910	BD251910 Compositi
2	642	100.0	642	6	AR258996	AR258996 Sequence
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4	642	100.0	642	6	AR371669	AR371669 Sequence
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6	642	95.5	642	6	AR259025	AR259025 Sequence
7	613.2	95.5	642	6	AR267498	AR267498 Sequence
8	613.2	95.5	642	6	AR371698	AR371698 Sequence
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10	613.2	95.5	2271	6	AX342535	AX342535 Sequence
11	613.2	95.5	2296	9	AF331844	AF331844 Homo sapi
12	613.2	95.5	2301	6	BD251906	BD251906 Compositi
13	613.2	95.5	2301	6	AR258992	AR258992 Sequence
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15	613.2	95.5	2301	6	AR371665	AR371665 Sequence
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17	613.2	95.5	2329	6	AX056687	AX056687 Sequence
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20	611.6	95.3	2301	6	BD251907	BD251907 Compositi
21	611.6	95.3	2301	6	BD251909	BD251909 Compositi
22	611.6	95.3	2301	6	AR258993	AR258993 Sequence
23	611.6	95.3	2301	6	AR258995	AR258995 Sequence
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27	611.6	95.3	2301	6	AR371668	AR371668 Sequence
28	610	95.0	2301	6	BD251908	BD251908 Compositi
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34	530	82.6	674	6	AR258998	AR258998 Sequence
35	530	82.6	674	6	AR267471	AR267471 Sequence
36	530	82.6	674	6	AR371671	AR371671 Sequence
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41	503.2	78.4	638	6	AR267470	AR267470 Sequence
42	503.2	78.4	638	6	AR371670	AR371670 Sequence
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44	461.4	71.9	532	4	AF326738	AF326738 Bos tauru
45	461.4	71.9	532	6	BD251913	BD251913 Compositi

ALIGNMENTS

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VERSION     BD251910.1  GI:3061680
KEYWORDS    JP 2002531090-A/5.
SOURCE      Cercopithecus pygerythrus
ORGANISM    Cercopithecus pygerythrus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Cercopithecus.
REFERENCE   1  (bases 1 to 642)
AUTHORS     Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
            Paeper,B.W., Ness,J.V. and Winkler,D.G.
TITLE       Compositions and methods for increasing bone mineralization
JOURNAL     Patent: JP 2002531090-A 5 24-SEP-2002;
            DARWIN DISCOVERY LTD
COMMENT     OS   Cercopithecus pygerythrus (vervet monkey)
            PN   JP 2002531090-A/5
            PD   24-SEP-2002
            PF   24-NOV-1999 JP 2000585404
            PR   27-NOV-1998 US 60/110283
            PI   MARY E BRUNKOW,DAVID J GALAS,BRIAN KOVACEVICH,JOHN T MULLIGAN,
            PI   BRYAN W PAEPER,JEFFREY VAN NESS,DAVID G WINKLER PC
            C12N15/09,C12N15/09,A01K67/027,A61K31/713,A61K48/00,A61P19/00, PC
            A61P19/02,
            PC   C07K14/47,C07K16/18,C07K19/00,C12N5/10,C12N9/00,C12P21/02, PC
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            Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   June 28, 2005, 15:05:42 ; Search time 2361.22 Seconds
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Perfect score:  642
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                Gapop 10.0 , Gapext 1.0
Searched:       3239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters:   68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	528	82.2	637	9	AY400963	AY400963 Pan trogl
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4	504.8	78.6	1990	6	AK017295	AK017295 Mus muscu
5	483.8	75.4	947	1	BY717106	BY717106
6	480	74.8	667	2	BB636457	BB636457 BB636457
7	458.2	71.4	623	2	BB637315	BB637315 BB637315
8	450.2	70.1	494	5	BX282099	BX282099 BX282099
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10	355.8	55.4	511	2	BB638050	BB638050 BB638050
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c 12	307.8	47.9	360	1	AI556282	AI556282 UI-R-C2p-
c 13	259	40.3	315	1	AI113131	AI113131 UI-R-C2p-
c 14	246.2	38.3	291	2	BE111224	BE111224 UI-R-BJ1-
c 15	208.8	32.5	535	8	AQ171546	AQ171546 HS_3088_B
16	158.4	24.7	532	1	AL922835	AL922835 AL922835
17	152.2	23.7	716	4	BJ712074	BJ712074 BJ712074
18	145.4	22.6	254	2	BF523030	BF523030 UI-R-C2p-
19	141	22.0	749	6	CA374043	CA374043 648343 NC
20	140.4	21.9	423	6	CB762755	CB762755 AMGNNUC:T
21	130.2	20.3	1880	3	CR681743	CR681743 Tetraodon
22	124.6	19.4	609	2	CR261683	CR261683 Reverse s
23	85.6	13.3	669	2	BF607657	BF607657 MY1_00059
24	84.2	13.1	854	6	BY707967	BY707967 BY707967
25	84.2	13.1	979	6	BY702931	BY702931 BY702931
26	84.2	13.1	988	6	BY702775	BY702775 BY702775
27	84.2	13.1	995	6	BY707897	BY707897 BY707897
28	84.2	13.1	1612	3	AK002396	AK002396 Mus muscu
29	84.2	13.1	1613	3	AK007893	AK007893 Mus muscu
30	84.2	13.1	1690	3	AK002240	AK002240 Mus muscu
31	84.2	13.1	1691	3	AK007967	AK007967 Mus muscu
32	83.4	13.0	575	7	CK625985	CK625985 mj16g02.y
33	83.4	13.0	621	7	CK626761	CK626761 mj25h07.y
34	82.4	12.8	584	7	CF169948	CF169948 B0820B07-
35	81.8	12.7	607	7	CF951492	CF951492 UI-M-HLO-
36	80.2	12.5	623	4	BI143761	BI143761 60907224
37	78.8	12.3	607	6	CA377916	CA377916 656613 NC
38	78.6	12.2	619	6	CB579051	CB579051 AMGNNUC:N
39	78.6	12.2	787	7	CO382488	CO382488 AGENCOURT
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41	78.2	12.1	723	4	BJ731200	BJ731200 BJ731200
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45	77.4	12.1	739	7	CK835725	CK835725 4060591 B

ALIGNMENTS

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VERSION     AY400962.1  GI:3975951
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 642)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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                    GenCore version 5.1.6
        Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      June 28, 2005, 14:54:42 ; Search time 373.896 Seconds
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Title:        US-10-788-606-9
Perfect score: 642
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Scoring table!: IDENTITY.NUC
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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36	613.2	95.5	2329	10	ADD90861	Add90861 Human CDN
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KW   osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
KW   BEER; gene therapy; antisense therapy; fracture; bone mineralization; ss.
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PA   (DARW-) DARWIN DISCOVERY LTD.
XX
PI   Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW;
PI   Van Ness J, Winkler DG;
XX
DR   WPI; 2000-412321/35.
DR   P-PSDB; AAY96431.
XX
PT   Nucleic acids (I) encoding a transforming growth factor beta binding
PT   protein, useful for identifying agents for treating osteopenia,
PT   osteoporosis and fractures.
XX
PS   Claim 1; Page 122; Page 122; 162pp; English.
XX
CC   This cDNA encodes a vervet transforming growth factor-beta (TGF-beta)
```

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    June 28, 2005, 15:15:06 ; Search time 429.419 Seconds
                              (without alignments)
                              9344.794 Million cell updates/sec

Title:        US-10-788-606-9
Perfect score: 642
Sequence:   1 atgcagctcccactggccct..........agctggagaacgcctactag 642

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters:      12134778

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	642	100.0	642	17	US-10-463-190-9	Sequence 9, Appli
3	642	100.0	642	17	US-10-464-368-101	Sequence 101, App
4	642	100.0	642	18	US-10-095-248A-9	Sequence 9, Appli
5	642	100.0	642	19	US-10-788-606-9	Sequence 9, Appli
6	642	100.0	642	21	US-10-799-162-9	Sequence 9, Appli
7	642	100.0	642	21	US-10-868-497-63	Sequence 63, Appl

8	613.2	95.5	642	16	US-10-384-893-45	Sequence 45, Appl
9	613.2	95.5	642	17	US-10-463-190-45	Sequence 45, Appl
10	613.2	95.5	642	17	US-10-464-368-10	Sequence 10, Appl
11	613.2	95.5	642	18	US-10-095-248A-45	Sequence 45, Appl
12	613.2	95.5	759	9	US-09-867-274-1	Sequence 1, Appli
13	613.2	95.5	2271	19	US-10-311-490A-1	Sequence 1, Appli
14	613.2	95.5	2301	16	US-10-384-893-1	Sequence 1, Appli
15	613.2	95.5	2301	17	US-10-463-190-1	Sequence 1, Appli
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17	613.2	95.5	2301	19	US-10-788-606-1	Sequence 1, Appli
18	613.2	95.5	2301	21	US-10-799-162-1	Sequence 1, Appli
19	613.2	95.5	2301	21	US-10-868-497-57	Sequence 57, Appl
20	613.2	95.5	2323	17	US-10-377-315-2	Sequence 2, Appli
21	613.2	95.5	2329	14	US-10-245-752-63	Sequence 63, Appl
22	613.2	95.5	2329	14	US-10-245-859-63	Sequence 63, Appl
23	613.2	95.5	2329	14	US-10-245-103-63	Sequence 63, Appl
24	613.2	95.5	2329	14	US-10-245-107-63	Sequence 63, Appl
25	613.2	95.5	2329	14	US-10-245-143-63	Sequence 63, Appl
26	613.2	95.5	2329	14	US-10-245-771-63	Sequence 63, Appl
27	613.2	95.5	2329	14	US-10-245-851-63	Sequence 63, Appl
28	613.2	95.5	2329	14	US-10-245-883-63	Sequence 63, Appl
29	613.2	95.5	2329	14	US-10-237-535-63	Sequence 63, Appl
30	613.2	95.5	2329	14	US-10-238-183-63	Sequence 63, Appl
31	613.2	95.5	2329	14	US-10-238-283-63	Sequence 63, Appl
32	613.2	95.5	2329	14	US-10-238-370-63	Sequence 63, Appl
33	613.2	95.5	2329	14	US-10-245-055-63	Sequence 63, Appl
34	613.2	95.5	2329	14	US-10-245-147-63	Sequence 63, Appl
35	613.2	95.5	2329	14	US-10-245-730-63	Sequence 63, Appl
36	613.2	95.5	2329	14	US-10-245-739-63	Sequence 63, Appl
37	613.2	95.5	2329	14	US-10-246-210-63	Sequence 63, Appl
38	613.2	95.5	2329	14	US-10-239-196-63	Sequence 63, Appl
39	613.2	95.5	2329	14	US-10-243-024-63	Sequence 63, Appl
40	613.2	95.5	2329	14	US-10-243-409-63	Sequence 63, Appl
41	613.2	95.5	2329	14	US-10-245-621-63	Sequence 63, Appl
42	613.2	95.5	2329	14	US-10-245-680-63	Sequence 63, Appl
43	613.2	95.5	2329	14	US-10-245-033-63	Sequence 63, Appl
44	613.2	95.5	2329	14	US-10-243-095-63	Sequence 63, Appl
45	613.2	95.5	2329	14	US-10-245-185-63	Sequence 63, Appl

ALIGNMENTS

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RESULT 1
US-10-384-893-9
; Sequence 9, Application US/10384893
; Publication No. US20030166247A1
; GENERAL INFORMATION:
;  APPLICANT: Brunkow, Mary E.
;  APPLICANT: Galas, David J.
;  APPLICANT: Kovacevich, Brian
;  APPLICANT: Mulligan, John T.
;  APPLICANT: Paeper, Bryan W.
;  APPLICANT: Van Ness, Jeffrey
;  APPLICANT: Winkler, David G.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
;  TITLE OF INVENTION:  BONE MINERALIZATION
;  FILE REFERENCE: 240083.508D5
;  CURRENT APPLICATION NUMBER: US/10/384,893
;  CURRENT FILING DATE:  2003-03-06
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 9
;  LENGTH: 642
;  TYPE: DNA
;  ORGANISM: Cercopithecus pygerythrus
US-10-384-893-9

  Query Match             100.0%;  Score 642;  DB 16;  Length 642;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-166;
  Matches  642;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         1 ATGCAGCTCCCACTGGCCCTGTCTGTTCTGCCTCGTCCTGGTACACCGAGCCTTCCGTGTA 60
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OM nucleic - nucleic search, using sw model

Copyright   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: June 28, 2005, 14:55:24 ; Search time 2782.85 Seconds
                                            (without alignments)
                                            9417.841 Million cell updates/sec

Title: US-10-788-606-9
Perfect score: 642
Sequence: 1 atgcagctcccactggccct........agctggagaacgcctactag 642

Scoring table: IDENTITY.NUC
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Searched: 4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   June 28, 2005, 14:55:24 ; Search time 451.701 Seconds
                                    (without alignments)
                          6348.430 Million cell updates/sec

Title:          US-10-788-606-9
Perfect score:  642
Sequence:       1 atgcagctcccactggcct.........agctggagaacgcctactag 642

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       13027057 seqs, 2233325459 residues

Total number of hits satisfying chosen parameters:     26054114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	544.2	84.8	570	15	US-60-677-583-99	Sequence 99, Appl
4	75.2	11.7	1089	15	US-60-680-544-23752	Sequence 23752, A
5	75.2	11.7	1089	15	US-60-680-473-23752	Sequence 23752, A
6	71	11.1	2337	1	PCT-US05-13260-1	Sequence 1, Appli
7	54.2	8.4	152132	11	US-10-940-774A-13845	Sequence 13845, A
8	54.2	8.4	152145	11	US-10-940-774A-12371	Sequence 12371, A
c 9	52.4	8.2	1917	9	US-10-703-032-28735	Sequence 28735, A
c 10	49.6	7.7	1149	7	US-10-990-000-13	Sequence 13, Appl
c 11	49.4	7.7	28493	13	US-11-031-175-1241	Sequence 1241, Ap
c 12	49.4	7.7	2323	11	US-10-990-328A-2709	Sequence 2709, Ap
c 13	49.4	7.7	2382	11	US-10-990-328A-2704	Sequence 2704, Ap
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c 17	49.4	7.7	25703	11	US-10-990-328A-97405	Sequence 97405, A
c 18	49.4	7.7	52112	11	US-10-990-328A-94429	Sequence 94429, A
c 19	48.6	7.6	1103	15	US-60-680-669-175-7216	Sequence 7216, Ap
c 20	48.6	7.6	10178	13	US-11-031-175-4897	Sequence 977, App
c 21	47.8	7.4	591	13	US-11-031-175-4897	Sequence 4897, Ap
22	47.8	7.4	2501	8	US-10-517-441-13	Sequence 13, Appl
23	47.8	7.4	9535	12	US-11-154-939-3030	Sequence 3030, Ap
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25	47.8	7.4	9535	15	US-60-664-936-1715	Sequence 1715, Ap
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; US-60-680-544-44583, Application US/60680544
; GENERAL INFORMATION:
;   APPLICANT: Cooper, Matthew
;   APPLICANT: Kinch, Deborah
;   APPLICANT: Rosenberg, Michael
;   APPLICANT: Subramaniam, S. Sai
;   APPLICANT: Szak, Suzanne
;   APPLICANT: Li, Huo
;   APPLICANT: Bandaru, Raj
;   APPLICANT: Derbel, Maher
;   TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
;   TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
;   FILE REFERENCE: 21590290000
;   CURRENT APPLICATION NUMBER: US/60/680,544
;   CURRENT FILING DATE: 2005-05-13
;   NUMBER OF SEQ ID NOS: 48714
;   SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 44583
;   LENGTH: 2302
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-60-680-544-44583

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              GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   June 28, 2005, 15:03:06 ; Search time 112.948 Seconds
                                     (without alignments)
                                     9300.665 Million cell updates/sec

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Perfect score: 642
Sequence:    1 atgcagctcccactggccct.........agctggagaacgcctactag 642

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:    1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:    2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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2	642	100.0	642	4	US-09-668-529A-9	Sequence 9, Appli
3	642	100.0	642	4	US-09-668-037A-9	Sequence 9, Appli
4	642	100.0	642	4	US-09-668-021-9	Sequence 9, Appli
5	613.2	95.5	642	3	US-09-449-218D-45	Sequence 45, Appl
6	613.2	95.5	642	4	US-09-668-529A-45	Sequence 45, Appl
7	613.2	95.5	642	4	US-09-668-037A-45	Sequence 45, Appl
8	613.2	95.5	2301	3	US-09-449-218D-1	Sequence 1, Appli
9	613.2	95.5	2301	4	US-09-668-529A-1	Sequence 1, Appli
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11	613.2	95.5	2301	4	US-09-668-021-1	Sequence 1, Appli
12	611.6	95.3	2301	3	US-09-449-218D-3	Sequence 3, Appli
13	611.6	95.3	2301	4	US-09-668-037A-7	Sequence 7, Appli
14	611.6	95.3	2301	4	US-09-668-529A-3	Sequence 3, Appli
15	611.6	95.3	2301	4	US-09-668-529A-7	Sequence 7, Appli
16	611.6	95.3	2301	4	US-09-668-037A-3	Sequence 3, Appli
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18	611.6	95.3	2301	4	US-09-668-021-3	Sequence 3, Appli
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25	530	82.6	674	4	US-09-668-529A-13	Sequence 13, Appl
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37	413.4	64.4	9301	4	US-09-668-529A-18	Sequence 18, Appl
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40	361	56.2	35828	3	US-09-449-218D-17	Sequence 17, Appl
41	361	56.2	35828	4	US-09-668-529A-17	Sequence 17, Appl
42	361	56.2	35828	4	US-09-668-037A-17	Sequence 17, Appl
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45	83.4	13.0	962	3	US-09-188-930-40	Sequence 40, Appl

ALIGNMENTS

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; Sequence 9, Application US/09449218D
; Patent No. 6395511
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
; TITLE OF INVENTION: BONE MINERALIZATION
; FILE REFERENCE: 240083.508
; CURRENT APPLICATION NUMBER: US/09/449,218D
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Cercopithecus pygerythrus
US-09-449-218D-9

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10741.894 Million cell updates/sec

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and is derived by analysis of the total score distribution.

SUMMARIES

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17	502	78.7	6	AX323453	AX323453 Sequence
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20	502	78.7	6	2301	BD251906	BD251906 Compositi
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22	502	78.7	6	2301	AR258992	AR258992 Sequence
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24	502	78.7	6	2301	AR267465	AR267465 Sequence
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26	502	78.7	6	2301	AR371665	AR371665 Sequence
27	502	78.7	6	2301	AR371667	AR371667 Sequence
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ALIGNMENTS

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VERSION   BD251911.1 GI:33061681
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  ORGANISM   Mus musculus
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              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 638)
  AUTHORS   Brunkow,M.E., Galas,D.J., Kovacevich,B.; Mulligan,J.T.,
              Paeper,B.W., Ness,J.V. and Winkler,D.G.
  TITLE   Compositions and methods for increasing bone mineralization
  JOURNAL   Patent: JP 2002531090-A 6 24-SEP-2002;
              DARWIN DISCOVERY LTD
OS   Mus musculus (mouse)
PN   JP 2002531090-A/6
PD   24-SEP-2002
PF   24-NOV-1999 JP 2000585404
PR   27-NOV-1998 US   60/110283
PI   MARY E BRUNKOW,DAVID J GALAS,BRIAN KOVACEVICH,JOHN T MULLIGAN,
PI   BRYAN E PAEPER,JEFFREY VAN NESS,DAVID G WINKLER PC
              C12N15/09,C12N15/09,A01K67/027,A61K31/713,A61K48/00,A61P19/00, PC
              A61P19/02,
PC   C07K14/47,C07K16/18,C07K19/00,C12N5/10,C12N9/00,C12P21/02, PC
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PC   C12Q1/02,C12Q1/68,G01N33/53,G01N33/53,G01N33/566,C12N15/00, PC
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PC   C12N5/00
CC   Compositions and methods for increasing bone mineralization FH
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ORIGIN

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    June 28, 2005, 15:05:42 ; Search time 2346.5 Seconds
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Title:          US-10-788-606-11
Perfect score:  638
Sequence:       1 atgcagccctcactagccc..........ctggagaacgcctactagag 638

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:        68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 7: gb_est7:*
                 8: gb_gss1:*
                 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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  8   416.4  65.3            637  9  AY400963  AY400963 Pan trogl
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 27   84.8  13.3  1612  3  AK000396  AK000396 Mus muscu
 28   84.8  13.3  1613  3  AK007893  AK007893 Mus muscu
 29   84.8  13.3  1690  3  AK002240  AK002240 Mus muscu
 30   84.8  13.3  1691  3  AK007967  AK007967 Mus muscu
 31   83.8  13.1   669  2  BF607657  BF607657 MTI_0059
 32   81.8  12.8   621  7  CK626761  CK626761 mj25h07.y
 33   80.8  12.7   472  2  BF420024  BF420024 UI-R-BJ2-
 34   80.8  12.7   532  2  BF407514  BF407514 UI-R-BJ2-
 35   80.8  12.7   575  7  CK625985  CK625985 mj16g02.y
 36   80.2  12.6   799  6  CD744251  CD744251 UI-M-AO0-
 37   79.8  12.5   385  7  AW434705  AW434705 UI-R-BJ0p
 38   79.8  12.5   584  7  CF169948  CF169948 B020E07-
 39   79.4  12.4   607  6  CA377916  CA377916 656613 NC
 40   79.2  12.4   607  7  CF951492  CF951492 UI-M-HL0-
 41   78    12.2   789  3  AK007935  AK007935 Mus muscu
 42   77.6  12.2   623  4  BI143761  BI143761 602907224
 43   77.4  12.1   723  4  BJ731200  BJ731200 BJ731200
 44   76.4  12.0   687  4  BI081999  BI081999 602879836
 45   75.8  11.9   739  7  CK835725  CK835725 4060591 B
```

(c markers appear at rows 10,13,14,18 and 36 in left margin)

ALIGNMENTS

```
RESULT 1
AK017295
LOCUS       AK017295               1990 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
            library, clone:5430411E23 product:sclerostin, full insert sequence.
ACCESSION   AK017295
VERSION     AK017295.1  GI:12856464
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE   99279253
   PUBMED    10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE   20499374
   PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE   20530913
   PUBMED    11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
```

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                  GenCore version 5.1.6
             Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      June 28, 2005, 14:54:42 ; Search time 371.567 Seconds
                                        (without alignments)
                              10164.517 Million cell updates/sec

Title:           US-10-788-606-11
Perfect score:   638
Sequence:        1 atgcagccctcactagcccc.........ctggagaacgcctactagag 638

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        439206 seqs, 295987067 residues

Total number of hits satisfying chosen parameters:      8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
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         2:  geneseqn1990s:*
         3:  geneseqn2000s:*
         4:  geneseqn2001as:*
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         9:  geneseqn2003bs:*
        10:  geneseqn2003cs:*
        11:  geneseqn2003ds:*
        12:  geneseqn2004as:*
        13:  geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	638	100.0	638	3	AAA29058	Aaa29058 Murine TG
2	638	100.0	638	13	ADS12968	Ads12968 TGF-beta
3	636	99.7	636	12	ADI27106	Adi27106 Mouse LRP
4	634.4	99.4	636	6	ABA94294	Aba94294 Mouse clo
5	634.4	99.4	636	10	ACF79826	Acf79826 Mouse SOS
6	607	95.1	675	12	ADI27108	Adi27108 Mouse LRP
7	556	87.1	674	3	AAA29059	Aaa29059 Rat TGF-b
8	556	87.1	674	10	ACF79827	Acf79827 Rat SOST
9	556	87.1	674	12	ADI27113	Adi27113 Rat LRP b
10	556	87.1	674	13	ADS12970	Ads12970 TGF-beta
11	503.2	78.9	642	12	AAA29057	Aaa29057 Vervet TG
12	503.2	78.9	642	12	ADI27200	Adi27200 Monkey LR
13	503.2	78.9	642	13	ADS12966	Ads12966 TGF-beta
14	502	78.7	759	6	ABA94293	Aba94293 Human clo
15	502	78.7	2271	6	AAD27576	Aad27576 Human ost
16	502	78.7	2301	3	AAA29056	Aaa29056 Human TGF
17	502	78.7	2301	3	AAA29055	Aaa29055 Human TGF
18	502	78.7	2301	13	ADS12958	Ads12958 TGF-beta
19	502	78.7	2301	13	ADS12962	Ads12962 TGF-beta
20	502	78.7	2323	10	ACF79824	Acf79824 Human SOS
21	502	78.7	2329	4	AAA91023	Aaa91023 Human sec
22	502	78.7	2329	6	ABK69992	Abk69992 cDNA enco
23	502	78.7	2329	9	ADA01331	Ada01331 Human PRO
24	502	78.7	2329	9	ADA43760	Ada43760 Human CDN
25	502	78.7	2329	9	ADA43528	Ada43528 Human PRO
26	502	78.7	2329	9	ADA01203	Ada01203 Human CDN
27	502	78.7	2329	9	ADA01087	Ada01087 Human PRO
28	502	78.7	2329	9	ADA43644	Ada43644 Human CDN
29	502	78.7	2329	9	ADA06906	Ada06906 Human PRO
30	502	78.7	2329	9	ADA08394	Ada08394 Novel hum
31	502	78.7	2329	9	ADB99687	Adb99687 Human PRO
32	502	78.7	2329	9	ADB86970	Adb86970 Human PRO
33	502	78.7	2329	9	ADB66125	Adb66125 Human CDN
34	502	78.7	2329	10	ADB99803	Adb99803 Human PRO
35	502	78.7	2329	10	ADB99458	Adb99458 Novel hum
36	502	78.7	2329	10	ADB66009	Adb66009 Human CDN
37	502	78.7	2329	10	ADC23407	Adc23407 Human CDN
38	502	78.7	2329	10	ADC26100	Adc26100 Human PRO
39	502	78.7	2329	10	ADE04927	Ade04927 Human PRO
40	502	78.7	2329	10	ADE11233	Ade11233 Human PRO
41	502	78.7	2329	10	ADD88164	Add88164 Human PRO
42	502	78.7	2329	10	ADD95459	Add95459 Human CDN
43	502	78.7	2329	10	ADE06389	Ade06389 Human PRO
44	502	78.7	2329	10	ADE38164	Ade38164 Human PRO
45	502	78.7	2329	10	ADD88280	Add88280 Human PRO

```
                              ALIGNMENTS

RESULT 1
AAA29058
ID   AAA29058 standard; cDNA; 638 BP.
XX
AC   AAA29058;
XX
DT   12-SEP-2000  (first entry)
XX
DE   Murine TGF-beta binding protein (BEER) cDNA.
XX
KW   osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
KW   BEER; gene therapy; antisense therapy; fracture; bone mineralization; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..636
FT                   /*tag= a
FT                   /product= "TGF-beta_binding_protein"
XX
PN   WO200032773-A1.
XX
PD   08-JUN-2000.
XX
PF   24-NOV-1999;  99WO-US027990.
XX
PR   27-NOV-1998;  98US-0110283P.
XX
PA   (DARW-) DARWIN DISCOVERY LTD.
XX
PI   Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW;
PI   Van Ness J, Winkler DG;
XX
DR   WPI; 2000-412321/35.
DR   P-PSDB; AAY96432.
XX
PT   Nucleic acids (I) encoding a transforming growth factor beta binding
PT   protein, useful for identifying agents for treating osteopenia,
PT   osteoporosis and fractures.
XX
PS   Claim 1; Page 123; 162pp; English.
XX
CC   This cDNA encodes a murine transforming growth factor-beta (TGF-beta)
```

```
                GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:  June 28, 2005, 15:15:06 ; Search time 426.743 Seconds
                                    (without alignments)
                          9344.794 Million cell updates/sec

Title:          US-10-788-606-11
Perfect score:  638
Sequence:       1 atgcagccctcactagcccc.........ctggagaacgcctactagag 638

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters:     12134778

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA:*
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   6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
   7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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  11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
  12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
  13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	638	100.0	638	16	US-10-384-893-11	Sequence 11, Appl
2	638	100.0	638	17	US-10-463-190-11	Sequence 11, Appl
3	638	100.0	638	18	US-10-095-248A-11	Sequence 11, Appl
4	638	100.0	638	19	US-10-788-606-11	Sequence 11, Appl
5	638	100.0	638	21	US-10-799-162-11	Sequence 65, Appl
6	638	100.0	638	21	US-10-868-497-65	Sequence 65, Appl
7	636	99.7	636	17	US-10-464-368-7	Sequence 7, Appli
8	634.4	99.4	636	9	US-09-867-274-3	Sequence 3, Appli
9	634.4	99.4	636	17	US-10-377-315-5	Sequence 5, Appli
10	607	95.1	675	16	US-10-464-368-9	Sequence 13, Appl
11	556	87.1	674	17	US-10-377-315-7	Sequence 13, Appl
12	556	87.1	674	17	US-10-463-190-13	Sequence 13, Appl
13	556	87.1	674	17	US-10-463-190-13	Sequence 14, Appl
14	556	87.1	674	18	US-10-464-368-14	Sequence 13, Appl
15	556	87.1	674	18	US-10-095-248A-13	Sequence 13, Appl
16	556	87.1	674	19	US-10-788-606-13	Sequence 13, Appl
17	556	87.1	674	21	US-10-799-162-13	Sequence 67, Appl
18	556	87.1	674	21	US-10-868-497-67	Sequence 101, App
19	503.2	78.9	570	17	US-10-463-190-101	Sequence 56, Appl
20	503.2	78.9	570	21	US-10-868-497-56	Sequence 9, Appli
21	503.2	78.9	642	16	US-10-384-893-9	Sequence 9, Appli
22	503.2	78.9	642	17	US-10-463-190-9	Sequence 101, App
23	503.2	78.9	642	17	US-10-464-368-101	Sequence 9, Appli
24	503.2	78.9	642	18	US-10-095-248A-9	Sequence 9, Appli
25	503.2	78.9	642	19	US-10-788-606-9	Sequence 9, Appli
26	503.2	78.9	642	21	US-10-799-162-9	Sequence 63, Appl
27	503.2	78.9	642	21	US-10-868-497-63	Sequence 1, Appli
28	502	78.7	759	9	US-09-867-274-1	Sequence 1, Appli
29	502	78.7	2271	19	US-10-311-490A-1	Sequence 5, Appli
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32	502	78.7	2301	17	US-10-463-190-1	Sequence 1, Appli
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38	502	78.7	2301	21	US-10-799-162-1	Sequence 5, Appli
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42	502	78.7	2323	17	US-10-377-315-2	Sequence 63, Appl
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45	502	78.7	2329	14	US-10-245-103-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-10-384-893-11
; Sequence 11, Application US/10384893
; Publication No. US20030166247A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
; TITLE OF INVENTION: BONE MINERALIZATION
; FILE REFERENCE: 240083.508D5
; CURRENT APPLICATION NUMBER: US/10/384,893
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-384-893-11

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Query Match             100.0%;  Score 638;  DB 16;  Length 638;
Best Local Similarity   100.0%;  Pred. No. 5.3e-164;
Matches 638;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 ATGCAGCCCTCACTAGCCCCGTGCCTCATCTGCCTACTTGTGCACGGTGCCTTCTGTGCT 60
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us-10-788-606-11.rnpm

Wed Jun 29 11:09:01 2005

OM nucleic - nucleic search, using sw model

Copyright GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: June 28, 2005, 14:55:24 ; Search time 2765.51 Seconds
                                            (without alignments)
                                 9417.841 Million cell updates/sec

Title: US-10-788-606-11
Perfect score: 638
Sequence: 1 atgcagccctcactagcccc..........ctggagaacgcctactagag 638

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Pending_Patents_NA_Main:*

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                    GenCore version 5.1.6

              Copyright (c) 1993 - 2005 Compugen Ltd.

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; GENERAL INFORMATION:
;  APPLICANT: Cooper, Matthew
;  APPLICANT: Kinch, Deborah
;  APPLICANT: Rosenberg, Michael
;  APPLICANT: Subramaniam, S. Sai
;  APPLICANT: Szak, Suzanne
;  APPLICANT: Li, Huo
;  APPLICANT: Bandaru, Raj
;  APPLICANT: Derbel, Maher
;  TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
;  TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
;  FILE REFERENCE: 21590290000
;  CURRENT APPLICATION NUMBER: US/60/680,544
;  CURRENT FILING DATE: 2005-05-13
;  NUMBER OF SEQ ID NOS: 48714
;  SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 44583
;  LENGTH: 2302
;  TYPE: DNA
;  ORGANISM: Homo Sapiens
US-60-680-544-44583

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          Copyright (c) 1993 - 2005 Compugen Ltd.

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6	556	87.1	674	4	US-09-668-529A-13	Sequence 13, Appl
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;  APPLICANT: Brunkow, Mary E.
;  APPLICANT: Galas, David J.
;  APPLICANT: Kovacevich, Brian
;  APPLICANT: Mulligan, John T.
;  APPLICANT: Paeper, Bryan W.
;  APPLICANT: Van Ness, Jeffrey
;  APPLICANT: Winkler, David G.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
;  TITLE OF INVENTION: BONE MINERALIZATION
;  FILE REFERENCE: 240083.508
;  CURRENT APPLICATION NUMBER: US/09/449,218D
;  CURRENT FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 45
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;  ORGANISM: Mus musculus
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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No: is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES

Result      Query
 No.  Score Match Length DB ID        Description
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  1    674  100.0   674   6 BD251912  BD251912 Compositi
  2    674  100.0   674   6 AR258998  AR258998 Sequence
  3    674  100.0   674   6 AR267471  AR267471 Sequence
  4    674  100.0   674   6 AR371671  AR371671 Sequence
  5    674  100.0   674  10 AF326741  AF326741 Rattus no
  6    674  100.0   674   6 AX323455  AX323455 Sequence
  7  557.6   82.7   636   6 BD251911  BD251911 Compositi
  8    556   82.5   638   6 AR258997  AR258997 Sequence
  9    556   82.5   638   6 AR267470  AR267470 Sequence
 10    556   82.5   638   6 AR371670  AR371670 Sequence
 11    556   82.5   638  10 AF326740  AF326740 Mus muscu
 12  536.2   79.6   759   6 AX323453  AX323453 Sequence
 13  536.2   79.6  2296   9 AF331844  AF331844 Homo sapi
 14  536.2   79.6  2301   6 BD251906  BD251906 Compositi
 15  536.2   79.6  2301   6 AR258992  AR258992 Sequence
 16  536.2   79.6  2301   6 AR267465  AR267465 Sequence
 17  536.2   79.6  2301   6 AR371665  AR371665 Sequence
 18  536.2   79.6  2323   9 AF326739  AF326739 Homo sapi
 19  536.2   79.6  2329   6 AX056687  AX056687 Sequence
 20  536.2   79.6  2329   6 AX574536  AX574536 Sequence
 21  536.2   79.6  2329   9 AY358627  AY358627 Homo sapi
 22  534.6   79.3  2301   6 BD251907  BD251907 Compositi
 23  534.6   79.3  2301   6 BD251909  BD251909 Compositi
 24  534.6   79.3  2301   6 AR258993  AR258993 Sequence
 25  534.6   79.3  2301   6 AR258995  AR258995 Sequence
 26  534.6   79.3  2301   6 AR267466  AR267466 Sequence
 27  534.6   79.3  2301   6 AR267468  AR267468 Sequence
 28  534.6   79.3  2301   6 AR371666  AR371666 Sequence
 29  534.6   79.3  2301   6 AR371668  AR371668 Sequence
 30    533   79.1  2301   6 BD251908  BD251908 Compositi
 31    533   79.1  2301   6 AR258994  AR258994 Sequence
 32    533   79.1  2301   6 AR267467  AR267467 Sequence
 33    533   79.1  2301   6 AR371667  AR371667 Sequence
 34  531.6   78.9  2271   6 AX342535  AX342535 Sequence
 35    530   78.6   642   6 BD251910  BD251910 Compositi
 36    530   78.6   642   6 AR258996  AR258996 Sequence
 37    530   78.6   642   6 AR267469  AR267469 Sequence
 38    530   78.6   642   6 AR371669  AR371669 Sequence
 39    530   78.6   642   9 AF326742  AF326742 Cercopith
 40  525.2   77.9   642   6 AR259025  AR259025 Sequence
 41  525.2   77.9   642   6 AR267498  AR267498 Sequence
 42  525.2   77.9   642   6 AR371698  AR371698 Sequence
 43  499.8   74.2  1154   9 AY358203  AY358203 Homo sapi
 44  428.2   63.5 226328   2 AC098160  AC098160 Rattus no
 45  428.2   63.5 236068   2 AC121721  AC121721 Rattus no
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                                                          ALIGNMENTS

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LOCUS       BD251912                   674 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Compositions and methods for increasing bone mineralization.
ACCESSION   BD251912
VERSION     BD251912.1  GI:3061682
KEYWORDS    JP 2002531090-A/7.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 674)
  AUTHORS   Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
            Paeper,B.W., Ness,J.V., and Winkler,D.G.
  TITLE     Compositions and methods for increasing bone mineralization
  JOURNAL   Patent: JP 2002531090-A 7 24-SEP-2002;
            DARWIN DISCOVERY LTD
OS          Rattus norvegicus (rat)
PN          JP 2002531090-A/7
PD          24-SEP-2002
PF          24-NOV-1999 JP 2000585404
PR          27-NOV-1998 US  60/110283
PI          MARY E BRUNKOW,DAVID J GALAS,BRIAN KOVACEVICH,JOHN T MULLIGAN,
PI          BRYAN W PAEPER,JEFFREY VAN NESS,DAVID G WINKLER PC
            C12N15/09,C12N15/09,A01K67/027,A61K31/713,A61K48/00,A61P19/00, PC
            A61P19/02,
PC          C07K14/47,C07K16/18,C07K19/00,C12N5/10,C12N9/00,C12P21/02, PC
            C12P21/08,
PC          C12Q1/02,C12Q1/68,G01N33/53,G01N33/566,C12N15/00, PC
            C12N15/00,
PC          C12N5/00
CC          Compositions and methods for increasing bone mineralization FH
            Key             Location/Qualifiers
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FT                          /organism='Rattus norvegicus (rat)'.
OS          Rattus norvegicus (rat)
FEATURES             Location/Qualifiers
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                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
ORIGIN
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OM nucleic - nucleic search, using sw model

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                      GenCore version 5.1.6
               Copyright (c) 1993 - 2005  Compugen Ltd.

Run on:        June 28, 2005, 15:05:42 ; Search time 2478.91 Seconds
                                          (without alignments)
                               10349.440 Million cell updates/sec

Title:          US-10-788-606-13
Perfect score:  674
Sequence:       1 gaggaccgagtgccctcct..........agctggagaacgcctactag 674
Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:    68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      EST:*
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                2: gb_est2:*
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                4: gb_est3:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_gss1:*
                9: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match %	Length	DB	ID	Description
1		570.2	84.6	1990	9	AK017295	AK017295 Mus muscu
2		557.6	82.7	636	3	AY400964	AY400964 Mus muscu
3		549.2	81.5	947	6	BY717106	BY717106 BY717106
4		542.2	80.4	667	2	BB636457	BB636457 BB636457
5		525.0	77.9	642	9	AY400962	AY400962 Homo sapi
6		518.8	77.0	623	2	BB637315	BB637315 BB637315
7		443.2	65.8	637	9	AY400963	AY400963 Pan trogl
8	c	419	62.2	419	2	BE101082	BE101082 UI-R-BJ1-
9		408.4	60.6	511	2	BB638050	BB638050 BB638050
10		382.8	56.8	494	1	BX282099	BX282099 BX282099
11	c	355.8	52.8	360	1	AI556282	AI556282 UI-R-C2p-
12		343.4	50.9	1177	3	AF184211	AF184211 Homo sapi
13	c	305.4	45.3	315	2	AI113131	AI113131 UI-R-C2p-
14	c	286.2	42.5	291	2	BE111224	BE111224 UI-R-BJ1-
15		218.2	32.4	254	2	BF523030	BF523030 UI-R-C2p-
16		199.4	29.6	423	8	CB762755	CB762755 AMGNNUC:T
17	c	167	24.8	535	4	AQ171546	AQ171546 HS_3088_B
18		152.2	22.6	716	4	BJ712074	BJ712074 BJ712074
19		152	22.6	532	2	AL922835	AL922835 AL922835
20		148.4	22.0	749	6	CA374043	CA374043 648343 NC
21		142	21.1	609	9	CR261683	CR261683 Reverse s
22		123.4	18.3	1880	3	CR681743	CR681743 Tetraodon
23		84.4	12.5	854	6	BY707967	BY707967 BY707967
24		84.4	12.5	979	6	BY702931	BY702931 BY702931
25		84.4	12.5	988	6	BY702775	BY702775 BY702775
26		84.4	12.5	995	6	BY707897	BY707897 BY707897
27		84.4	12.5	1612	3	AK002396	AK002396 Mus muscu
28		84.4	12.5	1613	3	AK007893	AK007893 Mus muscu
29		84.4	12.5	1690	3	AK002240	AK002240 Mus muscu
30		84.4	12.5	1691	3	AK007967	AK007967 Mus muscu
31		83.6	12.4	669	2	BF607657	BF607657 MY1_00059
32		82	12.2	472	2	BF420024	BF420024 UI-R-BJ2-
33		82	12.2	532	2	BF407514	BF407514 UI-R-BJ2-
34		82	12.2	575	7	CK625985	CK625985 mj16g02.y
35		82	12.2	621	7	CK626761	CK626761 mj25h07.y
36		81	12.0	385	2	AW434705	AW434705 UI-R-BJ0p
37		81	12.0	584	7	CF169948	CF169948 B0820E07-
38	c	80.4	11.9	607	6	CF951492	CF951492 UI-M-HL0-
39		80.2	11.9	799	6	CD742451	CD742451 UI-M-A00-
40		78.8	11.7	623	4	BI143761	BI143761 60290724
41		78	11.6	789	3	AK007935	AK007935 Mus muscu
42		77	11.4	723	4	BJ731200	BJ731200 BJ731200
43		76.4	11.3	687	4	BI081999	BI081999 60287983
44		75	11.1	355	1	AA197904	AA197904 mv05c05.r
45		75	11.1	433	1	AA067619	AA067619 mm23e07.r

ALIGNMENTS

```
RESULT 1
AK017295
LOCUS       AK017295                1990 bp    mRNA    linear    HTC 03-APR-2004
DEFINITION  Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
            library, clone:5430411B23 product:sclerostin, full insert sequence.
ACCESSION   AK017295
VERSION     AK017295.1  GI:12856464
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
  PUBMED    10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
  PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
  PUBMED    11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
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OM nucleic - nucleic search, using sw model

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          GenCore version 5.1.6
     Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: June 28, 2005, 14:54:42 ; Search time 392.533 Seconds
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Title: US-10-788-606-13
Perfect score: 674
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Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 439206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N Geneseq_16Dec04:*
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          4: geneseqn2001as:*
          5: geneseqn2001bs:*
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          9: geneseqn2003bs:*
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         11: geneseqn2003ds:*
         12: geneseqn2004as:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	674	100.0	674	3	AAA29059	Aaa29059 Rat TGF-b
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3	674	100.0	674	12	ADI27113	Adi27113 Rat LRP b
4	674	100.0	674	13	ADS12970	Ads12970 TGF-beta
5	557.6	82.7	636	6	ABA94294	Aba94294 Mouse clo
6	557.6	82.5	636	10	ACF79826	Acf79826 Mouse SOS
7	556	82.5	636	12	ADI27106	Adi27106 Mouse LRP
8	556	82.5	638	3	AAA29058	Aaa29058 Murine TG
9	556	82.5	638	13	ADS12968	Ads12968 TGF-beta
10	536.2	79.6	759	6	ABA94293	Aba94293 Human clo
11	536.2	79.6	2301	3	AAA29055	Aaa29055 Human TGF
12	536.2	79.6	2301	13	ADS12958	Ads12958 TGF-beta
13	536.2	79.6	2323	10	ACF79824	Acf79824 Human SOS
14	536.2	79.6	2329	4	AAA91023	Aaa91023 Human sec
15	536.2	79.6	2329	6	ABK69992	Abk69992 cDNA enco
16	536.2	79.6	2329	9	ADA01331	Ada01331 Human PRO
17	536.2	79.6	2329	9	ADA43760	Ada43760 Human CDN
18	536.2	79.6	2329	9	ADA43528	Ada43528 Human CDN
19	536.2	79.6	2329	9	ADA01203	Ada01203 Human PRO
20	536.2	79.6	2329	9	ADA01087	Ada01087 Human CDN
21	536.2	79.6	2329	9	ADA43644	Ada43644 Human CDN
22	536.2	79.6	2329	9	ADA06906	Ada06906 Human PRO
23	536.2	79.6	2329	9	ADA08394	Ada08394 Novel hum
24	536.2	79.6	2329	9	ADB99687	Adb99687 Human PRO
25	536.2	79.6	2329	9	ADB86970	Adb86970 Human PRO
26	536.2	79.6	2329	9	ADB66125	Adb66125 Human CDN
27	536.2	79.6	2329	10	ADB99803	Adb99803 Human PRO
28	536.2	79.6	2329	10	ADB99458	Adb99458 Novel hum
29	536.2	79.6	2329	10	ADB66009	Adb66009 Human CDN
30	536.2	79.6	2329	10	ADC23407	Adc23407 Human CDN
31	536.2	79.6	2329	10	ADC26100	Adc26100 Human PRO
32	536.2	79.6	2329	10	ADE04927	Ade04927 Human PRO
33	536.2	79.6	2329	10	ADE11233	Ade11233 Human PRO
34	536.2	79.6	2329	10	ADD88164	Add88164 Human PRO
35	536.2	79.6	2329	10	ADD95459	Add95459 Human CDN
36	536.2	79.6	2329	10	ADE06389	Ade06389 Human PRO
37	536.2	79.6	2329	10	ADE38164	Ade38164 Human CDN
38	536.2	79.6	2329	10	ADD88280	Add88280 Human PRO
39	536.2	79.6	2329	10	ADD90861	Add90861 Human CDN
40	536.2	79.6	2329	10	ADF99416	Adf99416 Human CDN
41	536.2	79.6	2329	10	ADG06509	Adg06509 Human PRO
42	536.2	79.6	2329	10	ADG05460	Adg05460 Human PRO
43	536.2	79.6	2329	10	ADG82461	Adg82461 Human PRO
44	536.2	79.6	2329	12	ADE51714	Ade51714 Human CDN
45	536.2	79.6	2329	12	ADE51830	Ade51830 Human CDN

ALIGNMENTS

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RESULT 1
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ID   AAA29059 standard; cDNA; 674 BP.
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AC   AAA29059;
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DT   12-SEP-2000  (first entry)
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DE   Rat TGF-beta binding protein (BEER) cDNA.
XX
KW   osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
KW   BEER; gene therapy; antisense therapy; fracture; bone mineralization; ss.
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OS   Rattus norvegicus.
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FH   Key             Location/Qualifiers
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FT                   /product= "TGF-beta_binding_protein"
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PN   WO200032773-A1.
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PD   08-JUN-2000.
XX
PF   24-NOV-1999;  99WO-US027990.
XX
PR   27-NOV-1998;  98US-0110283P.
XX
PA   (DARW-) DARWIN DISCOVERY LTD.
XX
PI   Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW;
PI   Van Ness J, Winkler DG;
XX
DR   WPI; 2000-412321/35.
DR   P-PSDB; AAY96433.
XX
PT   Nucleic acids (I) encoding a transforming growth factor beta binding
PT   protein, useful for identifying agents for treating osteopenia,
PT   osteoporosis and fractures.
XX
PS   Claim 1; Page 125; 162pp; English.
XX
CC   This cDNA encodes a rat transforming growth factor-beta (TGF-beta)
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:15:06 ; Search time 450.823 Seconds
                                        (without alignments)
                                        9344.794 Million cell updates/sec

Title: US-10-788-606-13
Perfect score: 674
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Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA:*
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        2: /cgm2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
        3: /cgm2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
        4: /cgm2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
        5: /cgm2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
        6: /cgm2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
        7: /cgm2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
        8: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
        9: /cgm2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
       10: /cgm2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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       16: /cgm2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
       17: /cgm2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
       18: /cgm2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
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       20: /cgm2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
       21: /cgm2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
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       24: /cgm2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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       26: /cgm2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

                              SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Match Length	DB	ID	Description
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2	674	100.0	674	17	US-10-377-315-7	Sequence 7, Appli
3	674	100.0	674	17	US-10-463-190-13	Sequence 13, Appl
4	674	100.0	674	17	US-10-464-368-14	Sequence 14, Appl
5	674	100.0	674	18	US-10-095-248A-13	Sequence 13, Appl
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7	674	100.0	674	21	US-10-799-162-13	Sequence 13, Appl
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26	536.2	79.6	2301	21	US-10-868-497-57	Sequence 57, Appl
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; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
; TITLE OF INVENTION: BONE MINERALIZATION
; FILE REFERENCE: 240083.508D5
; CURRENT APPLICATION NUMBER: US/10/384,893
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 45
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US-10-384-893-13

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SUMMARIES

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;  APPLICANT: Subramaniam, S. Sai
;  APPLICANT: Szak, Suzanne
;  APPLICANT: Li, Huo
;  APPLICANT: Bandaru, Raj
;  APPLICANT: Derbel, Maher
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Qy     74 ACATGCAGCCTTCGTTGCTGTGGAGAGCCAGGGGTGGCAAGCCTTCAAGAAATGATGCCAC 133
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       June 28, 2005, 15:03:06 ; Search time 118.578 Seconds
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Title:        US-10-788-606-13
Perfect score: 674
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              Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:     2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	Query Match %	Length	DB	ID	Description
1	674	100.0	674	3	US-09-449-218D-13	Sequence 13, Appl
2	674	100.0	674	4	US-09-668-529A-13	Sequence 13, Appl
3	674	100.0	674	4	US-09-668-037A-13	Sequence 13, Appl
4	674	100.0	674	4	US-09-668-021-13	Sequence 13, Appl
5	556	82.5	638	3	US-09-449-218D-11	Sequence 11, Appl
6	556	82.5	638	4	US-09-668-529A-11	Sequence 11, Appl
7	556	82.5	638	4	US-09-668-037A-11	Sequence 11, Appl
8	556	82.5	638	4	US-09-668-021-11	Sequence 11, Appl
9	536.2	79.6	2301	3	US-09-449-218D-1	Sequence 1, Appli
10	536.2	79.6	2301	4	US-09-668-529A-1	Sequence 1, Appli
11	536.2	79.6	2301	4	US-09-668-037A-1	Sequence 1, Appli
12	536.2	79.6	2301	4	US-09-668-021-1	Sequence 1, Appli
13	534.6	79.3	2301	3	US-09-449-218D-3	Sequence 3, Appli
14	534.6	79.3	2301	4	US-09-668-529A-3	Sequence 3, Appli
15	534.6	79.3	2301	4	US-09-668-529A-7	Sequence 7, Appli
16	534.6	79.3	2301	4	US-09-668-529A-7	Sequence 7, Appli
17	534.6	79.3	2301	4	US-09-668-037A-7	Sequence 7, Appli
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19	534.6	79.3	2301	4	US-09-668-021-3	Sequence 3, Appli
20	534.6	79.3	2301	4	US-09-668-021-7	Sequence 7, Appli
21	533	79.1	2301	3	US-09-449-218D-5	Sequence 5, Appli
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26	530	78.6	642	4	US-09-668-529A-9	Sequence 9, Appli
27	530	78.6	642	4	US-09-668-037A-9	Sequence 9, Appli

28	530	78.6	642	4	US-09-668-021-9	Sequence 9, Appl
29	525.2	77.9	642	3	US-09-449-218D-45	Sequence 45, Appl
30	525.2	77.9	642	4	US-09-668-529A-45	Sequence 45, Appl
31	525.2	77.9	642	4	US-09-668-037A-45	Sequence 45, Appl
32	424.6	63.0	532	3	US-09-449-218D-15	Sequence 15, Appl
33	424.6	63.0	532	4	US-09-668-529A-15	Sequence 15, Appl
34	424.6	63.0	532	4	US-09-668-037A-15	Sequence 15, Appl
35	424.6	63.0	532	4	US-09-668-021-15	Sequence 15, Appl
36	407.4	60.4	35828	3	US-09-449-218D-17	Sequence 17, Appl
37	407.4	60.4	35828	4	US-09-668-529A-17	Sequence 17, Appl
38	407.4	60.4	35828	4	US-09-668-037A-17	Sequence 17, Appl
39	407.4	60.4	35828	4	US-09-668-021-17	Sequence 17, Appl
40	372.6	55.3	9301	3	US-09-449-218D-18	Sequence 18, Appl
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42	372.6	55.3	9301	4	US-09-668-037A-18	Sequence 18, Appl
43	372.6	55.3	9301	4	US-09-668-021-18	Sequence 18, Appl
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45	82.8	12.3	962	3	US-09-188-930-40	Sequence 40, Appl

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                              ALIGNMENTS

RESULT 1
US-09-449-218D-13
; Sequence 13, Application US/09449218D
; Patent No. 6395511
; GENERAL INFORMATION:
;   APPLICANT: Brunkow, Mary E.
;   APPLICANT: Galas, David J.
;   APPLICANT: Kovacevich, Brian
;   APPLICANT: Mulligan, John T.
;   APPLICANT: Paeper, Bryan W.
;   APPLICANT: Van Ness, Jeffrey
;   APPLICANT: Winkler, David G.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
;   TITLE OF INVENTION: BONE MINERALIZATION
;   FILE REFERENCE: 240083.508
;   CURRENT APPLICATION NUMBER: US/09/449,218D
;   CURRENT FILING DATE: 1999-11-24
;   NUMBER OF SEQ ID NOS: 45
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 674
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-09-449-218D-13

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  Best Local Similarity  100.0%;  Pred. No. 9.7e-149;
  Matches  674;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy        301 CCGACGGCCCGTGCCCGAGTGCCAAGCCGGTCACCGAGTTGGTGTCGTGCTCGGGCCAGTGCG 360
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                        Copyright   GenCore version 5.1.6
                                    (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         June 28, 2005, 14:54:42 ; Search time 2399.78 Seconds
                                          (without alignments)
                                          10741.894 Million cell updates/sec

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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:       9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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               13: gb_un:*
               14: gb_vi:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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 3     532   100.0   532   6  AR258999  AR258999  Sequence
 4     532   100.0   532   6  AR267472  AR267472  Sequence
 5     532   100.0   532   6  AR371672  AR371672  Sequence
 6     467.9  87.9   642   6  AR259025  AR259025  Sequence
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 8     467.9  87.9   642   6  AR371698  AR371698  Sequence
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13     467.8  87.9  2301   6  BD251907  BD251907  Compositi
14     467.8  87.9  2301   6  AR258992  AR258992  Sequence
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16     467.8  87.9  2301   6  AR267465  AR267465  Sequence
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18     467.8  87.9  2301   6  AR371665  AR371665  Sequence
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25     466.2  87.6  2301   6  BD251909  BD251909  Compositi
26     466.2  87.6  2301   6  AR258994  AR258994  Sequence
27     466.2  87.6  2301   6  AR258995  AR258995  Sequence
28     466.2  87.6  2301   6  AR267467  AR267467  Sequence
29     466.2  87.6  2301   6  AR267468  AR267468  Sequence
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33     461.4  86.7   642   6  AR258996  AR258996  Sequence
34     461.4  86.7   642   6  AR267469  AR267469  Sequence
35     461.4  86.7   642   6  AR371669  AR371669  Sequence
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37     424.6  79.8   674   6  BD251912  BD251912  Compositi
38     424.6  79.8   674   6  AR258998  AR258998  Sequence
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45     414.2  77.9   638   6  AR258997  AR258997  Sequence
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ALIGNMENTS

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DEFINITION      Bos taurus sclerostin mRNA, partial cds.
ACCESSION       AF326738
VERSION         AF326738.1  GI:13161016
KEYWORDS        .
SOURCE          Bos taurus (cow)
  ORGANISM      Bos taurus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                Bovinae; Bos.
REFERENCE    1  (bases 1 to 532)
  AUTHORS       Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
                Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,
                Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,D.,
                Hamersma,H., Beighton,P. and Mulligan,J.T.
  TITLE         Bone dysplasia sclerosteosis results from loss of the SOST gene
                product, a novel cystine knot-containing protein
  JOURNAL       Am. J. Hum. Genet. 68 (3), 577-589 (2001)
   MEDLINE      21090529
   PUBMED       11179006
REFERENCE    2  (bases 1 to 532)
  AUTHORS       Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W.,
                Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J.,
                Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,D.,
                Hamersma,H., Beighton,P. and Mulligan,J.T.
  TITLE         Direct Submission
  JOURNAL       Submitted (07-DEC-2000) Genomics, Celltech Chiroscience Inc., 1631
                220th St. SE, Bothell, WA 98021, USA
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Wed Jun 29 11:09:06 2005

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                    GenCore version 5.1.6
           Copyright (c) 1993. - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       June 28, 2005, 15:05:42 ; Search time 1956.65 Seconds
                                 (without alignments)
                                 10349.440 Million cell updates/sec

Title:           US-10-788-606-15
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        3239544 segs, 1903213470 0 residues

Total number of hits satisfying chosen parameters:   68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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5	394.4	74.2	947	6	BY717106	BY717106 BY717106
6	391.4	73.6	623	2	BB637315	BB637315 BB637315
7	390.2	73.3	637	9	AY400963	AY400963 Pan trogl
c 8	355.8	66.9	419	2	BB101082	BB101082 UI-R-BJ1-
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c 13	263.8	49.6	315	1	AI113131	AI113131 UI-R-C2p-
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16	158.4	29.8	716	4	BJ712074	BJ712074 BJ712074
17	148.4	27.9	749	6	CA374043	CA374043 UI-R-BJ1-
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19	121.4	22.8	609	3	CR261683	CR261683 Reverse s
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c 21	95.2	17.9	669	2	BF607657	BF607657 MYI_00059
22	93	17.5	575	7	CK625985	CK625985 mj16g02.y
23	93	17.5	621	7	CK626761	CK626761 mj25h07.y
24	93	17.5	854	6	BY707967	BY707967 BY707967
25	93	17.5	979	6	BY702931	BY702931 BY702931
26	93	17.5	988	6	BY702775	BY702775 BY702775
27	93	17.5	995	6	BY707897	BY707897 BY707897
28	93	17.5	1612	3	AK002396	AK002396 Mus muscu
29	93	17.5	1613	3	AK007893	AK007893 Mus muscu
30	93	17.5	1690	3	AK002240	AK002240 Mus muscu
31	93	17.5	1691	3	AK007967	AK007967 Mus muscu
32	91.4	17.2	584	7	CF169948	CF169948 B0820E07-
33	91.4	17.2	607	7	CF951492	CF951492 UI-M-HL0-
34	89.8	16.9	623	4	BI143761	BI143761 602907224
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ALIGNMENTS

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DEFINITION Homo sapiens SOST gene, VIRTUAL TRANSCRIPT, partial sequence.
            genomic survey sequence.
ACCESSION   AY400962
VERSION   AY400962.1 GI:39756951
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 642)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 642)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
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            Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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COMMENT   This sequence was made by sequencing genomic exons and ordering
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Matches 500; Conservative   0; Mismatches 32; Indels 3; Gaps 1;

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    June 28, 2005, 14:54:42 ; Search time 309.833 Seconds
                                     (without alignments)
                              10164.517 Million cell updates/sec

Title:          US-10-788-606-15
Perfect score:  532
Sequence:       1 agaatgatgccacagaaatc.........accaaagccagccgcgggccga 532

Scoring table:  IDENTITY.NUC
                Gapop 10.0 , Gapext 1.0

Searched:       439206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:     8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     N_Geneseq_16Dec04:*
            1: geneseqn1980s:*
            2: geneseqn1990s:*
            3: geneseqn2000s:*
            4: geneseqn2001as:*
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            9: geneseqn2003bs:*
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           11: geneseqn2003ds:*
           12: geneseqn2004as:*
           13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES

Result         Query
No.    Score   Match Length DB ID          Description
------ ------  ----- ------ -- ------       -----------
   1    532   100.0   532    3 AAA29060     Aaa29060 Bovine TG
   2    532   100.0   532   12 ADI27209     Adi27209 Cow LRP b
   3    532   100.0   532   13 ADS12972     Ads12972 TGF-beta
   4    467.8  87.9   642    3 AAA94051     Aaa94051 Human DAN
   5    467.8  87.9   642   12 ADI27109     Adi27109 Human LRP
   6    467.8  87.9   759    6 ABA94293     Aba94293 Human clo
   7    467.8  87.9  2271    6 AAD27576     Aad27576 Human ost
   8    467.8  87.9  2301    3 AAA29061     Aaa29061 Mutant hu
   9    467.8  87.9  2301    3 AAA29055     Aaa29055 Human TGF
  10    467.8  87.9  2301   13 ADS12960     Ads12960 TGF-beta
  11    467.8  87.9  2301   13 ADS12958     Ads12958 TGF-beta
  12    467.8  87.9  2323   10 ACF79824     Acf79824 Human SOS
  13    467.8  87.9  2329    4 AAA91023     Aaa91023 Human sec
  14    467.8  87.9  2329    6 ABK69992     Abk69992 cDNA enco
  15    467.8  87.9  2329    9 ADA01331     Ada01331 Human PRO
  16    467.8  87.9  2329    9 ADA43760     Ada43760 Human CDN
  17    467.8  87.9  2329    9 ADA43528     Ada43528 Human CDN
  18    467.8  87.9  2329    9 ADA01203     Ada01203 Human PRO
  19    467.8  87.9  2329    9 ADA01087     Ada01087 Human CDN
  20    467.8  87.9  2329    9 ADA43644     Ada43644 Human CDN
  21    467.8  87.9  2329    9 ADA06906     Ada06906 Human PRO
  22    467.8  87.9  2329    9 ADA08394     Ada08394 Novel hum
  23    467.8  87.9  2329    9 ADB99687     Adb99687 Human PRO
  24    467.8  87.9  2329    9 ADB86970     Adb86970 Human PRO
  25    467.8  87.9  2329    9 ADB66125     Adb66125 Human cDN
  26    467.8  87.9  2329   10 ADB99803     Adb99803 Human PRO
  27    467.8  87.9  2329   10 ADB99458     Adb99458 Novel hum
  28    467.8  87.9  2329   10 ADB66009     Adb66009 Human CDN
  29    467.8  87.9  2329   10 ADC23407     Adc23407 Human CDN
  30    467.8  87.9  2329   10 ADC26100     Adc26100 Human PRO
  31    467.8  87.9  2329   10 ADE04927     Ade04927 Human PRO
  32    467.8  87.9  2329   10 ADE11233     Ade11233 Human PRO
  33    467.8  87.9  2329   10 ADD88164     Add88164 Human PRO
  34    467.8  87.9  2329   10 ADD95459     Add95459 Human cDN
  35    467.8  87.9  2329   10 ADE06389     Ade06389 Human PRO
  36    467.8  87.9  2329   10 ADE38164     Ade38164 Human PRO
  37    467.8  87.9  2329   10 ADD88280     Add88280 Human CDN
  38    467.8  87.9  2329   10 ADD90861     Add90861 Human cDN
  39    467.8  87.9  2329   10 ADF99416     Adf99416 Human PRO
  40    467.8  87.9  2329   10 ADG06509     Adg06509 Human PRO
  41    467.8  87.9  2329   10 ADG05460     Adg05460 Human PRO
  42    467.8  87.9  2329   10 ADG82461     Adg82461 Human PRO
  43    467.8  87.9  2329   12 ADE51714     Ade51714 Human cDN
  44    467.8  87.9  2329   12 ADE51830     Ade51830 Human cDN
  45    467.8  87.9  2329   12 ADE37688     Ade37688 Human cDN

                          ALIGNMENTS

RESULT 1
AAA29060
ID   AAA29060 standard; cDNA; 532 BP.
XX
AC   AAA29060;
XX
DT   12-SEP-2000  (first entry)
XX
DE   Bovine TGF-beta binding protein (BBER) cDNA.
XX
KW   osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
KW   BBER; gene therapy; antisense therapy; fracture; bone mineralization; ss.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..530
FT                   /tag= a
FT                   /partial
FT                   /product= "TGF-beta_binding_protein"
XX
PN   WO200032773-A1.
XX
PD   08-JUN-2000.
XX
PF   24-NOV-1999;  99WO-US027990.
XX
PR   27-NOV-1998;  98US-0110283P.
XX
PA   (DARW-) DARWIN DISCOVERY LTD.
XX
PI   Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW;
PI   Van Ness J, Winkler DG;
XX
DR   WPI; 2000-412321/35.
DR   P-PSDB; AAY96434.
XX
PT   Nucleic acids (I) encoding a transforming growth factor beta binding
PT   protein, useful for identifying agents for treating osteopenia,
PT   osteoporosis and fractures.
XX
PS   Claim 1; Page 126; 162pp; English.
XX
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OM nucleic - nucleic search, using sw model

Run on:      June 28, 2005, 15:15:06 ; Search time 355.843 Seconds
                                  (without alignments)
                          9344.794 Million cell updates/sec

Title:       US-10-788-606-15
Perfect score: 532
Sequence:    1 agaatgatgccacagaaatc.........accaaagccagccgggccga 532

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched:    6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters:     12134778

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA:*
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         5:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
         6:  /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
         7:  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
         8:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
         9:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
        10:  /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
        11:  /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
        12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
        13:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
        14:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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        23:  /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
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        25:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
        26:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match %	Query Length	DB	ID	Description
1	532	100.0	532	16	US-10-384-893-15	Sequence 15, Appl
2	532	100.0	532	17	US-10-463-190-15	Sequence 15, Appl
3	532	100.0	532	17	US-10-464-368-110	Sequence 110, App
4	532	100.0	532	18	US-10-095-248A-15	Sequence 15, Appl
5	532	100.0	532	19	US-10-788-606-15	Sequence 15, Appl
6	532	100.0	532	21	US-10-799-162-15	Sequence 15, Appl
7	532	100.0	532	21	US-10-868-497-69	Sequence 69, Appl
8			467.8	87.9	570	17	US-10-463-190-100	Sequence 100, App
9			467.8	87.9	570	21	US-10-868-497-55	Sequence 55, Appl
10			467.8	87.9	642	16	US-10-384-893-45	Sequence 45, Appl
11			467.8	87.9	642	17	US-10-463-190-45	Sequence 45, Appl
12			467.8	87.9	642	17	US-10-464-368-10	Sequence 10, Appl
13			467.8	87.9	759	18	US-10-095-248A-45	Sequence 45, Appli
14			467.8	87.9	759	9	US-09-867-274-1	Sequence 1, Appli
15			467.8	87.9	2271	19	US-10-311-490A-1	Sequence 1, Appli
16			467.8	87.9	2301	16	US-10-384-893-1	Sequence 3, Appli
17			467.8	87.9	2301	16	US-10-384-893-3	Sequence 3, Appli
18			467.8	87.9	2301	17	US-10-463-190-1	Sequence 1, Appli
19			467.8	87.9	2301	17	US-10-463-190-3	Sequence 3, Appli
20			467.8	87.9	2301	18	US-10-095-248A-1	Sequence 1, Appli
21			467.8	87.9	2301	18	US-10-095-248A-3	Sequence 3, Appli
22			467.8	87.9	2301	19	US-10-788-606-1	Sequence 1, Appli
23			467.8	87.9	2301	19	US-10-788-606-3	Sequence 3, Appli
24			467.8	87.9	2301	21	US-10-799-162-1	Sequence 1, Appli
25			467.8	87.9	2301	21	US-10-799-162-3	Sequence 3, Appli
26			467.8	87.9	2301	21	US-10-868-497-57	Sequence 57, Appli
27			467.8	87.9	2323	17	US-10-377-315-2	Sequence 2, Appli
28			467.8	87.9	2329	14	US-10-245-752-63	Sequence 63, Appl
29			467.8	87.9	2329	14	US-10-245-859-63	Sequence 63, Appl
30			467.8	87.9	2329	14	US-10-245-103-63	Sequence 63, Appl
31			467.8	87.9	2329	14	US-10-245-107-63	Sequence 63, Appl
32			467.8	87.9	2329	14	US-10-245-143-63	Sequence 63, Appl
33			467.8	87.9	2329	14	US-10-245-771-63	Sequence 63, Appl
34			467.8	87.9	2329	14	US-10-245-851-63	Sequence 63, Appl
35			467.8	87.9	2329	14	US-10-245-883-63	Sequence 63, Appl
36			467.8	87.9	2329	14	US-10-237-535-63	Sequence 63, Appl
37			467.8	87.9	2329	14	US-10-238-183-63	Sequence 63, Appl
38			467.8	87.9	2329	14	US-10-238-283-63	Sequence 63, Appl
39			467.8	87.9	2329	14	US-10-238-370-63	Sequence 63, Appl
40			467.8	87.9	2329	14	US-10-245-055-63	Sequence 63, Appl
41			467.8	87.9	2329	14	US-10-245-147-63	Sequence 63, Appl
42			467.8	87.9	2329	14	US-10-245-730-63	Sequence 63, Appl
43			467.8	87.9	2329	14	US-10-245-739-63	Sequence 63, Appl
44			467.8	87.9	2329	14	US-10-246-210-63	Sequence 63, Appl
45			467.8	87.9	2329	14	US-10-239-196-63	Sequence 63, Appl

ALIGNMENTS

```
RESULT 1
US-10-384-893-15
; Sequence 15, Application US/10384893
; Publication No. US20030166247A1
; GENERAL INFORMATION:
;   APPLICANT: Brunkow, Mary E.
;   APPLICANT: Galas, David J.
;   APPLICANT: Kovacevich, Brian
;   APPLICANT: Mulligan, John T.
;   APPLICANT: Paeper, Bryan W.
;   APPLICANT: Van Ness, Jeffrey
;   APPLICANT: Winkler, David G.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
;   TITLE OF INVENTION: BONE MINERALIZATION
;   FILE REFERENCE: 240083.508D5
;   CURRENT APPLICATION NUMBER: US/10/384,893
;   CURRENT FILING DATE: 2003-03-06
;   NUMBER OF SEQ ID NOS: 45
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
;   LENGTH: 532
;   TYPE: DNA
;   ORGANISM: Bos torus
US-10-384-893-15

Query Match           100.0%;  Score 532;  DB 16;  Length 532;
Best Local Similarity 100.0%;  Pred. No. 8.4e-134;
Matches   532;  Mismatches   0;  Conservative   0;  Indels   0;  Gaps   0;

Qy        1 AGAATGATGCCACAGAAATCATCCCGAGCTGGGCGAGTACCCGAGCCTGCCAGAGC 60
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                GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:      June 28, 2005, 14:55:24 ; Search time 2306.03 Seconds
                                        (without alignments)
                                        9417.841 Million cell updates/sec

Title:       US-10-788-606-15
Perfect score: 532
Sequence:    1 agaatgatgccacagaaatc.........accaaagccagccgggccga 532

Scoring table: IDENTITY_NUC
             Gapop 10.0 , Gapext 1.0

Searched:    45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters:        91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Pending_Patents_NA_Main:*
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        3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
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        5: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
        6: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
        7: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2005. Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          June 28, 2005, 14:55:24 ; Search time 374.306 Seconds
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Scoring table:   IDENTITY_NUC
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Searched:        13027057 seqs, 223325459 residues

Total number of hits satisfying chosen parameters:        26054114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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Result         %      Query
No.    Score   Match  Length  DB  ID                          Description
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  1    467.8   87.9    570    15  US-60-677-583-99             Sequence 99, Appl
  2    467.8   87.9   2302    15  US-60-680-544-44583          Sequence 44583, A
  3    467.8   87.9   2302    15  US-60-680-473-44583          Sequence 44583, A
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  7    54      10.2    927    13  US-11-031-175-9087           Sequence 9087, Ap
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c 19   48.4    9.1  11805   13  US-11-031-175-1016           Sequence 1016, Ap
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  32   47.2    8.9   2016    2  PCT-US05-06729-27            Sequence 27, Appl
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ALIGNMENTS

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; Sequence 99, Application US/60677583
; GENERAL INFORMATION:
; APPLICANT: Lu, Hsieng Sen
; APPLICANT: Paszty, Chris
; APPLICANT: Robinson, Martyn
; APPLICANT: Stephens, Paul Edward
; APPLICANT: Kirby, Hishani
; APPLICANT: Henry, Alistair James
; APPLICANT: Latham, John
; APPLICANT: Ramsdell, Fred
; APPLICANT: Winkler, David
; TITLE OF INVENTION: EPITOPES
; FILE REFERENCE: 60117-163
; CURRENT APPLICATION NUMBER: US/60/677,583
; CURRENT FILING DATE: 2005-05-03
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 99
;  LENGTH: 570
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-60-677-583-99

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Best Local Similarity  93.5%;  Pred. No. 5.7e-70;
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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:03:06 ; Search time 93.5954 Seconds
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Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	532	100.0	532	4	US-09-668-037A-15	Sequence 15, Appl
4	532	100.0	532	4	US-09-668-021-15	Sequence 15, Appl
5	467.8	87.9	642	3	US-09-449-218D-45	Sequence 45, Appl
6	467.8	87.9	642	4	US-09-668-529A-45	Sequence 45, Appl
7	467.8	87.9	642	4	US-09-668-037A-45	Sequence 45, Appl
8	467.8	87.9	2301	3	US-09-449-218D-1	Sequence 1, Appl
9	467.8	87.9	2301	4	US-09-449-218D-3	Sequence 3, Appli
10	467.8	87.9	2301	4	US-09-668-529A-1	Sequence 1, Appli
11	467.8	87.9	2301	4	US-09-668-529A-3	Sequence 3, Appli
12	467.8	87.9	2301	4	US-09-668-037A-1	Sequence 1, Appli
13	467.8	87.9	2301	4	US-09-668-037A-3	Sequence 3, Appli
14	467.8	87.9	2301	4	US-09-668-021-1	Sequence 1, Appli
15	466.2	87.6	2301	3	US-09-668-021-3	Sequence 3, Appli
16	466.2	87.6	2301	5	US-09-449-218D-5	Sequence 5, Appli
17	466.2	87.6	2301	3	US-09-449-218D-7	Sequence 7, Appli
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19	466.2	87.6	2301	4	US-09-668-529A-7	Sequence 7, Appli
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21	466.2	87.6	2301	4	US-09-668-037A-7	Sequence 7, Appli
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25	461.4	86.7	642	4	US-09-668-529A-9	Sequence 9, Appli
26	461.4	86.7	642	4	US-09-668-037A-9	Sequence 9, Appli
27	461.4	86.7	642	4	US-09-668-021-9	Sequence 9, Appli
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37	375.2	70.5	9301	4	US-09-668-529A-18	Sequence 18, Appl
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44	93	17.5	962	3	US-09-188-930-40	Sequence 40, Appl
45	93	17.5	962	3	US-09-188-930-209	Sequence 209, App

ALIGNMENTS

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; Sequence 15, Application US/09449218D
; Patent No. 6395511
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
; TITLE OF INVENTION: BONE MINERALIZATION
; FILE REFERENCE: 240083.508
; CURRENT APPLICATION NUMBER: US/09/449,218D
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Bos torus
US-09-449-218D-15

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Qy   301 ACTTCCGCTGCATCCCCGACCGCTACCCGCCGCGAGCCGTGTGTCCTGGCG 360